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Listing first 45 summaries
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ALIGNMENTS

RESULT AAX58986

AAX58986 standard; cDNA;

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CDS
WPI; 1999-371120/31
         Bradfield CA,
                          28-NOV-1997;
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                                    98WO-US25314
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MOP7; member of the PAS superfamily; bHLH-PAS; mouse; transcription regulator; hypoxia inducible factor 3 alpha; ss

Mouse transcription regulator MOP7 cDNA.

23-AUG-1999 AAX58986;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06295), a novel member of the PAS superfamily, where PAS stands of or PER/ARNT/SIM domains. The cDNA was identified in a search of murine ESTs designed to identify basic-helix-loop-helix-PAS (bHHH-PAS) proteins, and by RACE amplification of mouse lung cDNA. CC (MOP7 has been characterised as hypoxia inducible factor 3 alpha (See AAY06290), MOP3 (See CC (HIF 1 alpha (See AAY06289), HIF 2 alpha (See AAY06290), MOP3 (See CC (AAY06291), Ah receptor and Ah receptor nuclear translocator (ARNT), CC suggesting a different functional role. MOP7 probably regulates (the same genes as HIF 1 alpha and 2 alpha, as evidenced by its CC dimerisation with the same partners (ARNT, MOP3) and recognition (CC of the same core response element. MOP7 may have a functional CC role associated with response to low oxygen in the tissues in CC which it is expressed. The invention provides novel MOPS 2-9 nucleic acids (See AAX58891-88) and proteins (See AAX06289-97). CC These are useful in a variety of research, diagnostic and core applications. Several of the MOPs are alpha-class signal core and the mops are alpha-class signal core and the core are signal core.
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full-length chief in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a complementary to a polynucleotide comprises a 3'-end sequence, where the coligonucleotide comprises a 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13632 represent human cDNA sequences; AAB92446 to
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                               and/or diagnosis of the full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                                  SEQ ID 12421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                    invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                    ROM;
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RESULT
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AC AAH1
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 Human
                   26-JUN-2001
                                                         AAH17091
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                                                                                                     acaagccccctgcacagacttcccctgccgggagccctcgctccgagcctcccctgcaat
                                                                                                                                                                                                                              ccccaacagagcgccacttttccctgcgaatgaagagcacgctcaccagcagagggcgca
                                                                                                                                                                                                                                                                   aagaggaacttcaagacgccctgacccccaggccgaacctgtcaaagaagaagctggaag
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                                                                                                                                         acaagccacctgtgcagacttctccagctgggagccctgactcagagcccccgctgcagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612;
 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 79.9
12; Conservative
                                                         standard;
 sequence SEQ ID NO:16414
                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416
                  entry)
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79.98;
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Mismatches
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No. 8.
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CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the AH13628 and CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human cDNA sequences; AAB92446 to CC conservation of the protein sequences; AAB9245 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-ord primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide sequences at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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Wakamatsu
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ı A, Nagai K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense therapy; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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Sequence 2595 BP; 497 A; 897 Ç 703 ç; 498 Ŧ, 0 other;

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Length

Similarity

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Best Local S
Matches 583
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203
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        cgcacctggacaaggcctccatcatgcgcctcaccaatcagctacctgcgcatgcaccgcc
                                                        ggtcgaccacggagctgcgcaaggaaaagtcccgggatgcggcccgcagccggcgcagcc
                                                                                                        ggtcgaacaccgagctgcggaaggagaagtcgcgggacgcgggcccgcagccgccagcc
cccacctggacaaggcctctatcatgcgcctcaccatcagctacctgcgcatgcaccgcc
                                             aggagaccgaggtgctgtaccagctggctcacacgctgcccttcgcccgcggcgtcagcg
                                                                                                                                           Conservative
                                                                                                                                                    40.7%;
                                                                                                                                           0
                                                                                                                                         Score 447.4; DB:
Pred. No. 8.4e-83
0; Mismatches 71
                                                                                                                                           Indels
                                                                                                                                           70;
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tctgcgccgcagggagtggaaccaggtgggagcagggggagaaccactggatgcctgct

-agcaggtggaaaaagggggagagccactggacgcctgct

322

329

224

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RRESULT
AAHO7034
ID AAHH
XX AAHO7034
AC AAHC
AC AAHC
XX Huma
XX Huma
XX Huma
XX EP1C
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XX O7-F
XX 29-J
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                         Ota T,
Ishii
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                                     Isogai T,
Sugiyama
                                                                                                         HELIX
                                                                                                                                              99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                         RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
                                         Nishikawa
T, Wakama
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                                           Wakamatsu
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                                                             Hayashi
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                                                               Saito
                                         aito K,
Otsuki
                                                             Yamamoto
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primer sets for synthesizing polynucleotides, particularly tfull-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
                                                                                                                                                                  the 5602
ne detection
d by the
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Claim 1; SEQ ID 3869; 2537pp + G English

CC sequence and an oligonucleotide comprising a sequence complementary to a conjuncted which comprises a 3' end sequence, where the coligonucleotide which comprises a 3' end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5' end sequence/3' end sequence is selected from those defined in comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and comprise therapy. The primer sets can be used in antisense therapy and comprise the specification. The primer sets can be used in antisense therapy and comparison of the specific sets of the primers are also useful for the comparison of the full-length cDNAs. The primers allow obtaining of the full-length cC the full-length cDNAs. The primers allow obtaining of the full-length cC cDNAs easily without any specialised methods. AAH013166 to AAH13628 and CC AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention. The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-ord primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end eotides and γď ဇ္

Sequence 711 BP; 149 A; 239 c; 209 G; 111 Τ; w other

3.8; DB 3 4.7e-77;

22;

Length

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Best Local Similarity
Matches 581; Conserv 425 473 361 353 301 293 241 233 181 187 121 127 61 67 ட 7 ctggcgcacactctgccctttgcgcgcggggtcagcgcgcacctggacaaggcctccatc ggcacgagggccatggcgttgggggtgcagcgcgtgaggtcgaacaccgagctgcggaag aagaggagcttcaggacgccctgaccccccagcagaccctgtccaggaggaaggtggagg aagaggaacttcaagacgccctgacccccaggccgaacctgtcaaagaagaagctggaag ctgggcctcagtcagtggacctctgttcctcctccctgatacataaccccactcctggta ||||||||||||||| gagaagtcgcgggacgcggcccgcagccggcgcagccaggagacggaggtgctgtaccag gactggcgagccatggcgctggggctgcagcgccaaggtcgaccacggagctgcgcaag atgcgcctcacaatcagctacctgcgcatgcaccgcctctgcgc----ctggctcacacgctgcccttcgcccgcggcgtcagcgcccacctggacaaggcctctatc gaaaagtcccgggatgcggcccgcagccggcgcagccaggagaccgaggtgctgtaccag Conservative ctggagctcattggacacagcatctttgatttcatccacccctgtgacc Score 418.8; Pred. No. 4.7e 0; Mismatches 0; 84; Indels 73; ag Gaps 186 126 66 484 424 375 360 352 300 292 240 232 180 120 60 4:

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RESULT ARHO3708 ID ARHO3708 ID ARHO3708 ID ARHO 3708 ARHO ACC CONTICC 
The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set ccomprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cc complementary to a polynucleotide which comprises a 3'-end sequence complementary to a CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and Jor diagnosis of the abnormality of the proteins encoded by the
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full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis of the ength cDNAs -
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Sugiyama
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T, Wakama
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Wakamatsu
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RESULT
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Human cDNA sequence SEQ ID

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            ctcgctccgagcctccc--ctgcaatgcctggtgcttatc-tgtgaagccatcccccagc
                                                            ctgctcaggacatatgagggcctacaagcc-ccctgcacagacttcccctgccgggagcc
                                                                                                                cacgctcaccagcagagggcgcacgctcaacctcaaagcggccacctggaaggtgctgca
                                                                                                                                                                                                                                                                        gatacataaccccactcctggtaccaatttctctctctggagctcattggacacagtatctt
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cttgactcaaaacccccgnttgcantgcctggtgctcatcttgcgaagccattccccacc
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                                                ctgctctggacatatganggcctacaagccaccttgcgcagacttctccagctgggagcc
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Similarity 79.3%;
71; Conservative
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Pred. No. 1.1e-71;
Pred. No. 1.7e-71;
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the 502 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence which comprises a 5'-end cCC oligonucleotide comprises a 3'-end sequence, where the CCC oligonucleotide comprises a 1-end sequence, where the CCC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CCC the 5'-end sequence/3'-end sequence is selected from those defined in CCC the specification. The primers stress can be used in antisense therapy and CCC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length CCC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CCC AAB95893 represent human canid sequences; and AAH13629 to AAH13632 represent numan amino acid sequences; and AAH13629 to AAH13632 represent human canid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human canid sequences; and AAH13629 to AAH13632 represent human canid sequences; and AAH13629 to AAH13632 represent human canid sequences; and AAH13632 represent human canid sequences; and AAH13639 to AAH13639 represent human canid sequen
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Best Local Similarity
Matches 284; Conser
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonal-betide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets
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                                 cgccacttttccctgcgaatgaagagcacgctcaccagcagagggcgcacgctcaacctc
                                                                                                                                                         caagacgccctgacccccaggccgaacctgtcaaagaagcagcagcaggaagccccaacagag
                                                                                                                                                                                                                                                                                         cggtgcttctccttgcgcatgaagagtacgctcaccagccgcggggcgcaccctcaacctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for synthesizing polynucleotides, particularly the cDNAs defined in the specification, and for the detaction of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           23.0%;
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Wakamatsu
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Pred. No. 6.1e<sup>o</sup>
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L A, Nagai K
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No. 6.1e-43;
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RESULT
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Ishii
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                                                                                                                                                                                                                                                                                                                     primer;
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, Sugiyama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakama
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A, Nagai K,
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Otsuki
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs detection by the

Claim IJ 21; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which complementary to the the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers set scan be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13631 to AAH13632 t AAH13629 eotides

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Best Local Similarity 86.0
Matches 279; Conservative
                                                                                 Ota T
Ishii
       Primer sets for synthesizing polynucleotides, particularly full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
                                                                                                                                              11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                       07-FEB-2001
                                                                                                                                                                                                                                                                                 Human; primer;
                                                                                                                                                                                                                                                                                                     Human cDNA clone (5'-primer) SEQ ID NO:645.
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27-AUG-1999;
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, Sugiyama
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99JP-0300253.
2000JP-0118776.
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2000JP-0241899.
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                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy;
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                                                                                 Nishikawa T,
T, Wakamatsu
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Pred. No. 5.7e
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                                                                                Hayashi K, S
A, Nagai K,
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                                                                                Saito K,
(, Otsuki
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CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human canno acid sequences; AAB92446 to CC cof the present oligonucleotides, all of which are used in the exemplification CC of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 645; 2537pp + CD ROM;
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Sequence 733 143 A; 264 Ç 204 <u>:</u> 119 Ŧ; w other

Query Match Best Local Similarity

19.2%; 83.1%;

Score Pred.

211.6; DB No. 2e-34;

В

22; Length

733;

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                                                                    tacaagccccctgcacagacttcccctgccgggagccctcgctccgagcctcccctgcaa
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tgcctggtgctcatctgcgaagccatcccccacccaggcagcctggaggg
                                                      tacaagccacctgcgcagacttctccagctgggagccctgactcagagcccccgctgcag
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RESULT
AAH18364;
                 AAH18364 standard;
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                 CDNA; 1841
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AAH18364
ID AAH1
XX
AC AAH1
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DT 26-J
DT 26-J
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Hume
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Homc
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PF 28-;
XX
                                                               Human cDNA sequence
                                                                           26-JUN-2001
                                                                          (first
                                                               SEQ
                                                                          entry)
                                                               IJ
                                                               NO:18402
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Homo Human; primer; sapiens detection; diagnosis; antisense therapy; gene therapy;

SS

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07-FEB-2001

28-JUL-2000; 2000EP-0116126

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to the complementary strand of a polynucleotide which comprises one of consideration constructed constructions and of a polynucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the complementary to a polynucleotide comprises a 3'-end sequence, where the polynucleotide comprises as 3'-end sequence, where the specification. The primer sets can be used in antisense therapy and constitution of the specification. The primer sets can be used in antisense therapy and constitution and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the constant of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CAAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to CAAH3633 to AAH18741 human amino acid sequences; AAB92446 to constant of the constan
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1841
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                          tgcctggtgcttatctgtgaagccatcccccagctccccttccacgatgg
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tgcctggtgctcatctgcgaagccatcccccacccaggcagcctggaggg
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Wakamatsu
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Pred. No. 2.4e-34;
0; Mismatches 49
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1 A, Naga
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RESULT 10 AAX58981

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accagctggcgcacactctgccctttgcgcgcgcgtcagcgcgcacctggacaaggcct

ggaaggagaagtcgcgggacgcggcccgcagccggcggcagccaggaggacggaggtgctgt 121

4

ggaaggagaagtcccgggatgctgcggtgccggcggagcaaggagacggaggtgttct

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В
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Best Local Similarity
                                                                                                                                                                                                                                      or the Ah receptor nuclear translocator (ARNT). To obtain extended open reading frames for each EST, an anchored-PCR strategy was used to amplify additional flanking sequences from a commercial HepG2 library MOP2 appears to be related structurally and functionally to MOP1 (see AAY06289). It interacts with ARNT, but not AHR, and drives transcription in its ARNT-dimerised form. Unlike MOP1, it does not appear to interact significantly with HSP90. MOP2 is induced by low oxygen and may be involved in hypoxia responses in difference cells and tissues. MOP2 is sometimes referred to as hypoxia inducible factor 2 alpha. The invention provides novel
                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of a cDNA encoding MOP2 (see AAY06290), a novel member of the PAS superfamily, where PAS stands for PER/ARNT/SIM domains. The cDNA was identified in an iterative search of human ESTs designed to identify basic-helix-loop-helix-PAS (bHLH-PAS) proteins that interact with either the Ah receptor (AHR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                            MOPS 2-9 nucleic acids (see AAX908289-97).

These are useful in a variety of research, diagnostic and therapeutic applications. Several of the MOPs are alpha-class hypoxia-inducible factors. Others are involved in circadian signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 94-95; 106pp; English.
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               aattcggcacgaggccatggcgttggggctgcagcgcgtgaggtcgaaccaccgagctgc
                                                             446;
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                                                             Conservative
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57.5%;
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Pred. No. 1.1e-26;
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                                                                                                                                                   Endothelial PAS domain protein-1; EPAS1; angiogenes antiarteriosclerotic; antitumour; atherosclerosis; gene therapy; human; dominant negative mutant; ss.
         14-AUG-1998;
                            13-AUG-1999;
                                                                                                                         Synthetic
                                                                                                                                                                                          Human endothelial PAS domain protein-1 dominant negative
                                                                                                                                                                                                              05-JUN-2000
                                                                                                                                                                                                                                  AAZ94052;
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                                                                                                                                    Homo sapiens.
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The mutant lacks the transactivating domain (see AAY)9158) of the wild-type protein (see also AAY)9161). The invention is based on the discovery that EPAS1 binds to cis-acting regulatory sequences associated with genes encoding angiogenic factors such as vascular endothelial cell growth factor (VEGF) and VEGF receptors such as KDR/flk-1 and flt-1, thereby transactivating the promoters of such genes. A claimed method of inhibiting angiogenesis in a mammal comprises administering to the mammal a compound which inhibits binding of EPAS1 to the cis-acting transactivation regulatory DNA of an angiogenic factor (see AAZ94051). The compound may be an EPAS1 polypeptide lacking a transactivation domain or a nucleic acid encoding such a polypeptide. When such an EPAS1 mutant is bound to a cis-acting regulatory DNA, it prevents wild-type EPAS1 binding and thereby inhibits transcription of a gene encoding an angiogenic factor such as VEGF, and hence angiogenesis. The mutant is preferably administered to an atherosclerotic lesion or to a tumour site.

Angiogenesis is also inhibited using a compound, such as an EPAS1 compound to the procedular compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       damage, iscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulation of angiogenesis in mammals, useful for treating atherosclerosis, tumors, wounds, vascular disease, hypoxic damage, ischemia, balloon angioplasty, frostbite, gangrene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 4-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee
                                       EPAS-binding element, ARNT4 (see AAY79162).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present
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Sequence 1607 BP; 395 A; 480 C; 442 G; 290 T; 0 other;

15.7%;

DB 21; .1e-26;

Length 1607;

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RESULT 12
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                   protein 1 (EPASI). EPASI proteins can regulate specification of endothelial tissue, such as vasculature, the blood-brain barrier, etc. The protein can be used in a screening assay for agents that modulate binding of EPASI to a binding target, especially a basic helix-loop-helix (bHLH)/PAS protein, a heat shock protein or hypoxia inducible factor (HIF-I alpha) binding site. The EPASI protein is inducible factor (HIF-I alpha) binding site.
                                                                                                                                                                                                                                                                                                      Endothelial PAS domain protein 1 proteins regulators, e.g. a heat shock protein
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hes 445; Conservative
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RESULT 1 AAZ94053 ID AAZ9

13

AAZ94053

standard; cDNA;

2818

ВP

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CKDR/filk-1 and filt-1, thereby transactivating the promoters of such as genes. A claimed method of inhibiting angiogenesis in a mammal comprises administering to the mammal a compound which inhibits binding of EPAS1 to the cis-acting transcription regulatory DNA of an angiogenet factor (see AAZ94051). The compound may be an EPAS1 polypeptide lacking a transactivation domain (see AAY79160) or a nucleic acid encoding such a polypeptide, an antisense nucleic acid complementary to mRNA encoding EPAS1, or an EPAS1-specific antibody. The compound is preferably administered to an atherosclerotic The compound is preferably administered to an atherosclerotic acid compound, such as an EPAS1 dominant negative mutant, which inhibits binding of EPAS1 to the EPAS-binding element, ARNT4 (see AAY79162). Angiogenesis can be promoted by administering EPAS1 DNA to increase expression of VEGF or VEGF receptor in endothelial cells of a
Query Match
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Matches 445
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of cDNA encoding human endothelial PA domain protein-1 (EPASI, see AAV79161). The invention is based or the discovery that EPASI binds to cis-acting regulatory sequences associated with genes encoding angiogenic factors such as vascular endothelial cell growth factor (VEGF) and VEGF receptors such as
                                                                                                                   patient suffering from peripheral vascular disease, cerebral vascular disease, hypoxic tissue damage (e.g. hypoxic damage heart tissue), or coronary vascular disease as well as to tre patients who have, or have had, translent ischaemic attacks, vascular graft surgery, balloon angioplasty, frostbite, gangr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       damage,
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antiarteriosclerotic; antitumour; atherosclerosis; tumour;
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ABA14358 standard; DNA; 32169 ВÞ

23-JAN-2002 (first entry)

system related polynucleotide SEQ Ħ ö

RESULT 1
ABA14358
ID ABA1
XX ABA1
XX ABA1
XX Huma
DE Huma
XX Huma
KW Inmmu
KW anti
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulni antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological Human; nootropic; neuroprotective; cytostatic; suppressive; antiinflammatory; anti-HIV; disease; infection; gene dermatological; cancer; vaccine; vulnerary; ds

Conservative

Indels

85;

Gaps

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31-JAN-2000

31-JAN-2000

24-FEB-2000

12-MAR-2000

11-MAR-2000

11-MAR-2000

11-JUL-2000

11-AUG-2000

11-SEP-2000

11-SEP-2000
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03-CT 2000
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RESULT 1
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Matches 185
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                                                                                                                                                                                                                        Differential expression; polymorphism; biological pathway; IRES; GFP; ss; internal ribosome entry site; green fluorescent protein; EPAS1; human; hypoxia regulated gene; macrophage; endothelial PAS domain protein 1;
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hypoxia regulated
HIF-2 alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for preventing, cancers and metastases
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No. 4.1e-26;
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atctttctgtcagaaaacatcagcaagttcatgggacttacacag------
                  aacttgtacctgaaagccttggagggtttcattgccgtggtgacccaagatggcgacatg
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58.4%;
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3.7e-26;
hes 220;
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Search completed: September 8, 2002, 06:49:31 Job time: 6984 sec

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Result
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Maximum Match 100%
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Perfect score:
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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Sequence 1, Appli	Ñ	3-08-185-414E-1	1 US	630		

RESULT
US-08-78
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; Patent
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; APP
; APP ; TOPOLOGY: 1; MOLECULE TYPE: US-08-785-241-1 TELEPHONE: (415) 343-43.
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36, SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
COLLENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TELECOMMUNICATION INFORMATION: TITLE OF INVENTION: STRANDEDNESS: APPLICATION NUMBER: US/08/785,241 FILING DATE: 17-JAN-1997 CLASSIFICATION: 435 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS TYPE: nucleic acid REFERENCE/DOCKET NUMBER: UTSD:1229 ZIP: 94104 COUNTRY: LENGTH: 2816 base pairs USA linear Endothelial PAS Domain Protein 36,627 Version #1.30

Query Match 15.7%; Score 173; DB 1; Length 2816;
Best Local Similarity 57.4%; Pred. No. 7.9e-32;
Matches 445; Conservative 0; Mismatches 245; Indels 85; Gaps

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ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V(
                                                                                                                                                                                                                                                        Sequence 2, Application US/08785241 Patent No. 5695963
                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MCKNight, Steven L.
APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
TITLE OF INVENTION: Endothelial PAS
NUMBER OF SEQUENCES: 7
                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                             COUNTRY:
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                                                                                                          CALIFORNIA
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REFERENCE/DOCKET NUMBER: UTSD;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341;
TELEPHONE: (415) 343-4342;
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3031 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-785-241-2
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Best Local Similarity 57.1%;
Matches 441; Conservative
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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                                                            agaagctggaagccccaacagagcgccacttttccctgcgaatgaagagcacgctcacca
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                     gtgaccaagaggaacttcaagacgccctgaccccca----ggccgaacctgtcaaaga
                                                                                                                                                                                                                                                                                                                                      GGTTTCATTGCTGTGGTGACCCAAGACGGTGACATGATCTTTCTGTCGGAAAACATCAGC
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   GGCAAGTGAGAGTCTACAACAACTGCCCCC---CTCACAGTAGCCTCTGTGGCTCCAAGG
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Best Local Similarity
Matches 387; Conserv
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3736 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-19:
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                  ccctggagggtttcgtcatggtactcaccgccgagggagacatggcttacctgtcggaaa
                                                                                                         CTGGTGATTTGGATATTGAAGATGACATGAAAGCACAGATGAATTGCTTTTATTTGAAAG
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                                                     CCTTGGATGGTTTTGTTATGGTTCTCACAGATGATGGTGACATGATTTACATTTCTGATA
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T: 4225 Executive Square, Suite 1400
La Jolla
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)N: 514
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HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
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Patent No. 6020462
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                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             NAME: Haile, Lisa A.
REGISTON NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616
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CITY: I
STATE:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        TOPOLOGY:
                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                            TYPE:
                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/915,213
20-AUG-1997
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Score 134.6; DB 3; Pred. No. 1e-22; """ matches 244;
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Matches 387; Query Match Best Local

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Length 3736; Indels

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Query Match
Best Local Similarity
                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: Hypoxia Inducible Factor-1
FILE REFERENCE: 07265/151001
CURRENT APPLICATION NUMBER: US/09/148,547
CURRENT FILLING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                          SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                    Sequence 1, Application Patent No. 6124131
                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(2509)
-09-148-547-1
                                                                                                               ORGANISM: Homo
                                                                                                                               TYPE: DNA
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No. 1e-22;
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GENERAL INFORMATION:
APPLICANT: Semenz.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,21
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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FILING DATE: CLASSIFICATION:

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Best Local Similarity 54.7%;
Matches 387; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3736 base pairs
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APPLICATION NUMBER:
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Pred. No. 1e-22
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1
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Best Local Similarity
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TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3736 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/10251 FILING DATE: 06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STRANDEDNESS: single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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            ccccactcctggtaccaatttctctctggagctcattggacacagtatcttttgattttat 458
                                                       ATGTGAACAAATACATGGGATTAACTCAGT --
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US-08-785-310A-1
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                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/785
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2078 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
115 gtgctgtaccagctggcgcacactctgccctttgcgcgcggcgtcagcgcgcacctggac 174
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                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                  STRANDEDNESS:
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                                                 9a9Ct9C9gaa9gagaa9tC9C9ggaC9C9gCCCGCagCCG9gC9CCagCCaggagaCggag 114
                              cagcagagggggcacgctcaaacctcaaaggggccacctggaaggtgctgcactgctcagg 638
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                                                                                                          Score 89.6; DB 2;
Pred. No. 3.3e-12;
                                                                                           Mismatches
                                                                                                                      Length 2078;
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                                                                                                                                                                                                                                                           Query Match 6.5%;
Best Local Similarity 62.0%;
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,6
REFERENCE/DOCKET NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341
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 370
                                                            310
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-JAN-1997
                                                                                                       430 AAGGCTTCCATCGTGCGCCTCAGCGTCACCTACCTCCGCCTGCGCCGGTTCGCCGCGCTG 489
                                                                                                                                                                                      55 gagctgcggaaggagaagtcgcgggaacgcggcccgcagcaggcgcagcaggagacggag 114
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AAGGCGTCCATCGTGCGTCTTAGCGTCACCTACCTCCGCCTGCGTCGTTTTGCCGCGCTG 369
                                    aaggcctccatcatgcgcctcacaatcagctacctgcgcatgcaccgcctctgcgcagca 234
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.7e-08;
0; Mismatches 70;
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us-08-955-918C-1

Sequence 1, Application Patent No. 6268130 GENERAL INFORMATION:

Application US/08955918C

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Query Match
Best Local Similarity
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; LOCATION:
US-08-955-918C-1
                                                                                                                                    RESULT 11
US-08-738-349-1
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                                                                                                     Sequence 1, Application US/08738349 Patent No. 5869638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/697
ETILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGENT INFORMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (61),227,7400
                                                                        GENERAL INFORMATION: Takesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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 TITLE OF INVENTION:
                                             APPLICANT:
                                                            APPLICANT:
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                 APPLICANT:
                               APPLICANT:
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                                                                                                                                                                                                                                                                        STRANDEDNESS:
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EDNESS: single
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VENTION: RP Compositions and Therapeutic
VENTION: Diagnostic Uses Therefor
                                         Okazaki, Makoto
Kawai, Shinji
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                       Takeshita, Sunao
               Amann, Egon
                            Tsujimura, Atsushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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79.8%;
Bone-Related Cadherin-Like Protein and
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Pred. No. 2.4e-06;
1; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                             Length 2184;
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Best Local Similarity
"~+~hes 73; Conserva
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                                                                                                                                                                          US-08-722-126A-4
                                                                                                                                       Sequence 4, Application US/08722126A
Patent No. 6034227
                                         GENERAL INFORMATION:
APPLICANT: PECHY, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MARA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
NAME: Barker, M. P.
22,013
                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RCLEASE #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Process for Its Production NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      3546 AAAAAAAAAAAAAAAAAAAAAGCGGCCGC 3575
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LENGTH: 3581 base pair
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                               NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER:
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1300 I Street,
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BROWDY AND NEIMARK, P.L.L.C.
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81.1%;
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Pred. No. 8.6e-06;
0; Mismatches 17;
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Best Local Similarity
                                                                                                                                                                                                                                            Sequence 4, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A
TITLE OF INVENTION: FU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                            STATE:
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FILING DATE: 06-APR-1995
                                                                                         COUNTRY:
                                                                                                                                         STREET:
                                                                                                                                                         ADDRESSEE:
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BROWDY, Roger L.
BROWDY, Roger L.
25,618
                                                                                                           D.C.
                                                                                                                                      E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
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                                                                                             USA
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SYSTEM: PC-DOS/MS-DOS
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71.3%;
                                                                                                                                                                                                A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
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Pred. No. 8.4e-06;
0; Mismatches 33;
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; Sequence 71, Application US/09227357
; Patent No. 6342581
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PCT-US95-04258-4
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Best Local Similarity
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EARLIER
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CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
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                               EARLIER
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
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NAME/KEY:
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PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: (
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STRANDEDNESS: single
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
FILING DATE: 1997-07-08
                             APPLICATION NUMBER: 60/051,916 FILING DATE: 1997-07-08
                                                                                                                              APPLICATION NUMBER: 60/052,732 FILING DATE: 1997-07-08
                                                                                                                                                              APPLICATION NUMBER: 60/052,803 FILING DATE: 1997-07-08
                                                                                                                                                                                                 APPLICATION NUMBER: 60/051,929 FILING DATE: 1997-07-08
                                                                                                                                                                                                                                APPLICATION NUMBER: 60/051,925 FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/051,930 FILING DATE: 1997-07-08
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71.3%;
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Pred. No. 8
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FILING DATE:

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; NAME/KEY: SITE
; LOCATION: (410)
; OTHER INFORMATION: n
US-09-227-357-71
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                                                                                         Query Match
Best Local Similarity
Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1997-09-1
EARLIER APPLICATION NUMBER: 60
EARLIER FILING DATE: 1997-09-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1997-09-12 NUMBER OF SEQ ID NOS: 672
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                            APPLICATION NUMBER: 60/058,785
FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,664
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/058,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 1997-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-08-18
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/055,948
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APPLICATION NUMBER: 60/055,723
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Pred. No. 6.4e-06;
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Search completed: September Job time: 6385 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 Patent No.
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 205-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                 1509
                                                                                1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEVERIES:
CORRESPONDENCE ADDRESS:
BIRCH, STEWART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN)
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375
                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: FALLS CHURCH
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PO BOX 747
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AWS20329 UI-R-BUOP
AWS20329 UI-R-BUOP
AI712316 UI-R-AP1AV322372 AV322372
AI578946 UI-R-AA0AU118844 AU118844
AI510204 mj02902.y
BF654229 3278403 MA
BM483179 536412 MA
AL544018 AL544018
BF548129 UI-R-A0-b
AW133666 fi10c03.y
BM133666 fi10c03.y
BM13266 fi10c03.y
BM13266 fi20c03.y
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BE721988 189855 MA
BM182143 fv54b05.y
AK017853 Mus muscu
BE721988 189855 MA
BM182186 fv62h07.y
AK0132294 AU132294
BG772697 602720844
AW211226 U12920844
AW211226 U12920849
BM157049 fc55e08.y

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AI322407 mi19b08 y
AL528423 AL528423
AL519496 AL519496
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AL541807 AL541807
BG699633 602679365
AU118510 AU118510
AA028416 mi19b08 r
BH772109 603059192
AA041707 mj02g02 r
BM118906 L0917H03-
BM118909 L0917H06-
BM118909 L0917H06-
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                                                                                                                                                                                                                                                        Description
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COMMENT
                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
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DEFINITION
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VERSION
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Other_ESTs: mab24h10.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
CDNA Library Preparation: M. Bent
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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/tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
                                         /db_xref="taxon:10090"
/clone="IMAGE:3971562"
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EST 03-JAN-2001 s cDNA clone

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Fatima

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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:277775
MGI:277775
This read is a RESEQUENCE of a previously sequenced
This read has been verified (found to hit its origin
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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//db_xref="taxon:10090"
//clone="IMAGE:463959"
//clone=lib="Soares mouse p3NNFI9.5"
//dev_stage="19.5 dpc total fetus"
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                                                                                            gagggccatggcgttggggctgcagcgcgtgaggtcgaacaccgagctgcggaaggagaa 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcacactctgccctttgcgcgcggcgtcagcgcgcacctggacaaggcctccatcatgcg 191
                                          9tcgcgggacgcggccgcagccagccaggagacggaggtgctgtaccagctggc 131
                          GTCCCGGGATGCGGCCGCAGCCGGCGCA--CAGGAGACCGAGGTGCTGTACCAGCTGGC 119
                                                                              GCGAGCCATGGCGCTGGGGCTGCAGCGCGCAAGGTCGACCACGGAGCTGCGCAAGGAAAA 61
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AL528423 LTI_NFL003_NBC3
prime, mRNA sequence.
AL528423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 905)
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Eukaryota; Metazoa;
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EST.
                                                                                                                                                 Similarity
                                                                                                                                                                                                                      183
                                                                                                                                     Conservative
                                                                                                                                                                                                             /lab_host="pH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"

83 a 302 c 273 g 145 t . 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="neuroblastoma cells"
                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="LTI_NFL003_NBC3"
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="CS0DC029YH22"
                                                                                                                                               40.9%;
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Primates;
                                                                                                                                  Score 449.6; DB 9; Pred. No. 9.1e-47; l; Mismatches 75;
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Li,W.B., Gruber,C., Jessee,J. and Full-length cDNA libraries and norn Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Seq.
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Wel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cctcacaatcagctacctgcgcatgcaccgcctctgcgc-----
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                                                                                                                                                                                                                                                                                                                                                    prime, mRNA
AL519496
AL519496.1
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Eukaryota; Mutheria; Primates;
                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 856)
Li,W.B., Gruber,C.,
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                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence
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/tissue_type="neuroblastoma/lab_host="DH10B"
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                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                       GI:12782989
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Homo sapiens
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                                                                                                                                             Web : www.genoscope.cns.
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                                                                                        ctgtgaagccatcccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCGAASCATCCCCC 678
                                                                                                                                     GCAGACTTCTCCAGCTGGGAGCCCTGACTCAGAGCCCCCGCTGCAGTGCCTGGTGCTCAT
                                                                                                                                                     acagacttcccctgccgggagccctcgctccgagcctcccctgcaatgcctggtgcttat
                                                                                                                                                                                                       GGCGGCCACCTGGAAGGTGCTGAACTGCTCTGGACATATGAGGGCCTACAAGCCACCTGC
                                                                                                                                                                                                                         agcggccacctggaaggtgctgcactgctcaggacatatgagggcctacaagccccctgc
                                                                                                                                                                                                                                                                         GTGCTTCTCCTTGCGCATGAAGAGTACACTCACCAGCCGCGGGCGCACCCTCAACCTCAA
                                                                                                                                                                                                                                                                                       ccacttttccctgcgaatgaagagcacgctcaccagcagaggggggcacgctcaacctcaa
                                                                                                                                                                                                                                                                                                                                           GGACGCCCTGACCCCCAGCAGACCCTGTCCAGGAGGAAGGTGGAGGCCCCCACGGAGCG
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                                                                                                    741
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Pred. No. 3.6e
1; Mismatches
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3.6e-46;
nes 73;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CS0DE007YA24"
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                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Libzary Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
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1 (bases 1 to 767)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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602679365F1 NIH_MGC_95 Homo
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High quality sequence stop: 616.
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         /note-*Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-Xhol (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGXI, National Institutes of Health). Note: this is a NIH_MGC Library." a 259 c 242 g 110 t
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                                    Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. an
                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 756)
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             ctgctcaggacatatgagggcctacaagcc-ccctgcacagacttcccctgccgggagcc 688
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CTGCTCTGGACATATGANGGCCTACAAGCCACCTTGCGCAGACTTCTCCAGCTGGGAAGCC
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1532-3 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Contact: Takao Isc
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/clissue_type="whole embryo, mainly head"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/dev_stage="embryo, 10 weeks"
/note="Vector: pMEL8SFL3"
/note="Vector: pMEL8SFL3"
123 t 4 other
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/clone="HEMBA1003760"
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actetgecetttgegegegegteagegegeacetggaeaaggeeteeateatgegeete 195
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AA028416
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Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Du
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996
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142 c 131 g 88 t 3 others
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96.1%;
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B1772109
B1772109.1 GI:
                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 633)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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603059192F1 NIH_MGC_122
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Plate: LLAM11523 row: g column:
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                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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             119
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Location/Qualifiers
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             þ
                                                 primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                        /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5208622"
/clone_lib="NIH_MGC_122"
             (Invitrogen). Research Genetics tracking this is a NIH_MGC Library." 225 c 189 g 100 t
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                                                                                                                                                            Unpublished (1996)
Contact: Marra W/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 459)
1 (bases 1 to 459)
Nammalia; Eutheria; Louis (bases 1 to 459)
1 (bases 1 to 459
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
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                                                               musculus cDNA clone LO9
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BM118906.1 GI:17086932
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    Location/Qualifiers
         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 418)
                                          Mus musculus
                                                                                                 L0917H03-3 NIA Mouse Newborn musculus cDNA clone L0917H03
                                                       house mouse.
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 Kargul, G.J.,
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/strain="C57BL/6J"
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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 Dudekula,D.B.,
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                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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TAGCCCAGAAACCCACAAATGTCTCCAAAACCACCATAAAGACCTCTCCTTGTTAGGCAC
                                                                 CCCTTAACCGGAAAAATTGTCCTGGCTAGGAGGGAGGGAAGGACATGGCCCAGCTATCCT
                                                                                   cccttaaccggaaaaattgtcctggctaggagggagtgaagggacatggcccagctatcct
                                                                                                                                    CTGTTCAGGTGCTACAGGGGAAAGGGACTGAATCCTCTCTCCCCTCATGGGTGTTGTGGG
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plate: L0917 row: H column: 03
Seq.primer: -21M13 Forward
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Systematic Analyses of NIA Mouse Newborn Kidney cDNA Library
Unpublished (2001)
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: kidney; Vector: pSPORT1 (Invitrogen);
Site_1: SalI; Site_2: NotI; Mouse cDNA project by the
Laboratory of Genetics, National Institute on Aging (NIA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intramural Research Program, NIH
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/tissue_type="Newborn Kidney"
/dev_stage="Newborn"
/lab_host="DH10B"
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/strain="C57BL/6J"
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Pred. No. 4.8e-28;
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Plate: L0917 row: H column: 06
Seq primer: -21M13 Forward
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National Institute on Aging/National Institutes of Health
National Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Ko,M.S.H. Systematic Analyses of NIA Mouse Newborn Kidney cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 425)
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                                                                                                                       microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes, and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao (NIA)." 95 a 96 c 136 g
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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/lab_host="DH10B"
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/tlssue_type="Newborn Kidney"
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/db_xref="taxon:10090"
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                   27.1%;
99.0%;
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Score 298.2; DB 10;
Pred. No. 4.8e-28;
0; Mismatches 3;
  Indels
                                         Length 425;
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L0929A01-3 NIA Mouse Newborn
musculus cDNA clone L0929A01
BM119659 GI:17087685
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0929 row: A column: 01
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Systematic Analyses of NIA Mouse Newborn Kidney cDNA Library
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop:
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                                                       note="Organ: kidney; Vector: pSPORTI (Invitrogen);
Site_1: Sall; Site_2: Noti; Mouse cDNA project by the
Laboratory of Genetics, National Institute on Aging (NIA),
Intramural Research Program, NIH
(http://lgsun.grc.nia.nih.gov/cDNA). This is a
long-transcript enriched cDNA library (Ref. Genome Res.
11:1553-1558 (2001). [PMID:11544199]). In brief
/clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long)"
/tissue_type="Newborn Kidney"
/dev_stage="Newborn"
                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="niaEST:L0929A01-3"
/db_xref="taxon:10090"
                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                    /clone="L0929A01
                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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                                       double-stranded cDNAs were synthesized with an Oligo(dT)
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Kidney cDNA Library (Long) Mus
3', mRNA sequence.
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                                                                                                                                                                      l (bases 1 to 396)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                         BF653212 396 bp mRNA linear
276910 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF653312
BF653212.1 GI:11918281
                                                                                                                                                                                                                                                                                                                                                                                             EST
USDA, ARS, US Meat Animal PO Box 166, Clay Center, 1 Tel: 402 762 4366 Fax: 402 762 4390
                                                                             Contact: Smith TPL
                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute. Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                 Genome Res. 11 (4),
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626-630 (2001)
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Pred. No. 4.4e-28;
                                      NE 68933-0166, U
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320; Conservative
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AU116888.1
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AU116888
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COUNTRY COlumn; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 68 row: F column: 23
Seq primer: ATTTAGGTGACACTATAG.
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            Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
                                         Eukaryota;
Mammalia; I
                                                                  Homo sapiens
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Yamamoto,J.,
                                                                                   numan
                                                                                                                                        sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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/lab_host="DH10B"
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                          1 to 873)
                                          Eutheria;
                                                       Metazoa;
 Wakamatsu, A., Nakamura, Y.,
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Primates;
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iens cDNA
                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                      mRNA linear EST 19-OCT-2000 clone HEMBA1000216 5', mRNA
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    Nagai,T.,
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    Sugano, S. and
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Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genomics@hri.co.jp
HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
305 c 248 g 142 t 3 other
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/db_xref="taxon:9606"
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JOURNAL PUBMED REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT AF416641 DEFINITION TITLE TITLE Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1032)
Makino, Y., Cao, R., Svensson, K., Bertilsson, G., Asman, M., Tanaka, H.,
Cao, Y., Berkenstam, A. and Poellinger, L.
Inhibitory PAS domain protein is a negative regulator of hypoxia-inducible gene expression
Nature 414 (6863), 550-554 (2001) 2 (bases 1 to 1032)
Makino,Y., Cao,R., Sve
Cao,Y., Berkenstam,A.
Direct Submission AF416641 AF416641.1 GI:17432318 AF416641 1032 bp Mus musculus inhibitory PAS domain 11734856 house mouse. Svensson, K., Bertilsson, G., Asman, M., Tanaka, H., A. and Poellinger, L. protein (Ipas) mRNA, complete mRNA linear ROD 09-DEC-2001

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/protein_id="AAL39015.1"
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PRPNLSKKKLBAPTERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQT
SPAGSPRSEPPLQCLVLLCBALTQLPFHDGATLGLPQEKTPISTLFTPLMKALLCLVK
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Gu,Y.Z., Moran,S.M., Hogenesch,J.B., Wartman, Direct Submission
Submitted (16-APR-1998) Oncology, University University Avenue, Madison, WI 53706, USA
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/product="hypoxia inducible factor three alpha"
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Hif-3a gene; hypoxia indonway rat.
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ALAQSSEDKGLELIEIKPPKRSPRLEPGSFLLPPLSLSFLLQGRQLLGNQQDPRAPLV
HSHEPLGLAPSLLSLCQHEETVQPRNHFPPAAGLGQTH"
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Submitted (05-MAY-2000) Kietzmann T., Biochemistry I, I
Biochemistry and Molecular Cell Biology, Humboldtallee
Goettingen, GERMANY
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//db_xref="STTREMBL:QJHS2"
//db_xref="STTREMBL:QJHS2"
//translation="MMDQDRSSTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARG
//translation="MMDQDRSSTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARG
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DMAYLSENVSKHIGLSQLELIGISIFDETHPCOGELQDALTPRSLSKKSEAARGR
HFSLRWKSTLTSRGRALNLKAATWKVLHCSGHWRAYKPPAQTSPAGSPRSEPPLCCLV
LICEAIPHPASLEPPLGRGAFLSRHSLDMKFTYCDERIAEVAGYSPDDLIGCSAYEYI
HALDSDAVSRS.HTLLSKGQAVTGQYRFLARTGGYLWTGQATVVSGGRGGPSESIIC
VHFLISRYEENGVVLSLEQTEQHTRPPQLGTSSKKGIPGNSLDPPAPRILAFLHPA
LSEASLAADPRRFCSPDLRRLMAPILDFPQLGTSSKKGIPGNSLDPPAPRILAFLHPA
LSEASLAADPRRFCSPDLRTLMAPILDFPTAAPTSTPQAARRPQSPLPADLPDQLAV
GLENAHRLSTAAKKKTWETDLDIAQDPDTPDLEMLAPYISMDDDGPLNSSEQLPKVHR
RPPRTARRPRARSFHGLSPPIPEATPLLPRWGSDPRLNGSSPSKGDPTAPLTPRRRKR
ALAQSSEDKGLELLETKPPKRSPRLEPGSVLPPLSLSFILQGRQLPGNQPDPRAPLV
DSHEPLGLAPSLLSLYQHEETIQSRNHFLPAAGLAQTH"

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/protein_id="CAB96611.1"
/db_xref="GI:8953575"
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/tissue_type="liver"
/dev_stage="adult"
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/db_xref="taxon:10116"
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                            Submitted (10°MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                AK027725 2082 bp mRNA linear Homo sapiens cDNA FLJ14819 fis, clone OVARC1000241, similar to HYPOXIA-INDUCIBLE FACTOR 1 ALPHA.
                     University of Tokyo.
                                                                                                                                             Direct Submission
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Isogai,T. and Otsuki,T.
                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                              Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimor Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S.,
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/clone_lib="OVARC1"
/note="cloning vector: pME18SFL3"
13. .1911
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/db_xref="taxon:9606"
/clone="OVARC1000241"
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Direct Submission
Over 27-DEC-2001) Pathology,
Submitted (27-DEC-2001) Pathology,
Downs Blvd., MDC11,
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HPPSLSEAALAADPRRFCSPDLRRLLGFILDGASVAATPSTPLATRHPQSPLSADLPD
ELPVGTENVHRLFTSGKDTEAVETDLDIAQDAALDLEMLAFYISMDDDFQLNASEQL
PRAYHRPLGAVVRPRAKSFHGLSPPALEPSLLPRWGSDPRLSCSSPSRGDPSASSPMA
GARKRTILAQSSEDEDEGVELLGVRPPKRSPSPEHENFLLFPLSLVCWGINGILWPSLP
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/protein_id="AAL69947.1"
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RGVSAHLDKASIMRLTISYLRMHRLCAAGEWNOVGAGGEPLDACYLKALEGFVMVLTA
EGDMAYLSENVSKHLGLSQLELIGHSITEDIHPCDQEELQDALTPQQOTLSRRKVEAPT
ERGDMAYLSENVSKHLGLSQLELIGHSITEDIHPCDQEELQDALTPQQOTLSRRKVEAPT
ERGDMAYLSENVSKHLGLSQLELIGHSITEDIHPCDQEELQDALTPQQTSPAGSPDSEPPDQ
ERCESLEMKSTLTSRGTLNLKAATWKVLNCSGHMRAYKPAQTYSPAGTSDESPPDQ
LVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCDDRIAEVAGYSPDDLIGCSAYE
YIHALDSDANSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVYSGGRGDSESSIT
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/db_xref="taxon:9606"
/chromosome="19"
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21458277
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Hara, S., Kobayashi, C., Hamada, J. and Imura, N. Direct Submission Submitted (15-JAN-2001) Shuntaro Hara, Kitasato University, School of Pharmaceutical Sciences; 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan (E-mail:haras@pharm.kitasato-u.ac.jp, Tel:81-3-5791-6265, Fax:81-3-3442-4146)
                                                                                                                                                                               Hara,S., Hamada,J., Kobayashi,C., Kondo,Y. and Imura,N. Expression and characterization of hypoxia-inducible factor (HIF)-3alpha in human kidney: suppression of HIF-mediated generates by HIF-Jalpha
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CTCCTTGCGCATGAAGAGTACGCTCACCAGCCGCGGGCGCACCCTCAACCTCAAGGCGGC
                                                                                                     CCTGACCCCCAGCAGACCCTGTCCAGGAGGAAGGTGGAGGCCCCCACGGAGCGGTGCTT
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//codon_start=1
//protein_id="hypoxia-inducible factor-3 alpha"
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//protein_id="hypoxia-inducible factor-3 alpha"
//db_xref="GI:16040975"
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/db_xref="taxon:9606"
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0; Mismatches 85; Indels 7
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1 sogai, T. and Otsuki, T.
1 sogai, Helix Research Institute,
2 submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
3 submitted (23-AUG-2000) Takao Isogai, Chiba 292-0812, Japan
3 sequencis Laboratory; 152-3 Yana, Kisarazu, Chiba 292-0812, Japan
3 sequencing Leboratory; 152-3 Yana, Kisarazu, Chiba 292-0812, Japan
4 sequencing CNA sequencing project supported by Ministry of Takao Institute (supported by Japan Key Technology; Conter
4 sequencing Si-6 3 Sequencing and clone selection:
4 Helix Research Institute (supported by Japan Key Technology Center
4 sequencing and Department of Virology, Institute of Medical Science,
1 institute of Takao
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1 (sogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakawi,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T. NEDO human cDNA sequencing project
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Homo sapiens embryo, 10 weeks whole embryo,
mRNA, clone_lib:HEMBA1 clone:HEMBA1003760.
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                                             TAEGDMAYLSENVSKHLGLSQLELIGHSIFDFIHPCDOEELQDALTPQOTLSRRKVEA
PTERCFSLRMKSTLTSRGRTLNLKAATWKVLNCSGHWRAYKPPAQTSPAGSPDSEPPL
QCLVLLCEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCDDRIAEVAGYSPDDLIGCSA
YEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLMTQTQATVVSGGRGPQSE
SICVCHIFLISRVEETGVVLSLEQTEQHSRRPIQRGAPSQKDFENGDSLTDFQFRILA
FLHPPSLSEAALAADPRRFCSPDLRRLLGPILDGASVAATPSTPLATRHPQSPLSADL
PDELPYGTENVHRLFTSGKDTEAVETDLDIAQDADALDLEMLAPYISHDDDFQLNASE
                                                                                                                                                                                                                                                                                                                                                                                   /note="cloning vector: 226. 2172
QLPRAYHRPLGAVPRPRARSFHGLSPPALEPSLLPRWGSDPRLSCSSPSRGDPSASSP
MAGARKRTLAQSSEDEDEGVELLGVRPPKRSPSPEHENFLLFPLSLSFLLTGGPAPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
/dev_stage="embryo, 10 weeks"
                                                                                                                                                                                                                                          /protein_id="BAB13865.1"
/db_xref="GI:10432879"
/translation="MRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYLKALEGFVMVL
                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="HEMBA1003760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Eutheria; Primates; Catarrhini;
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Best Local Similarity
Matches 583; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               acctgaaggccctggagggtttcgtcatggtactcaccgccgagggagacatggcttacc
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        AC073814
AC073814.2 GI:9256812
HTG; HTGS_PHASE2; HTGS_DRAFT
                                 pieces
                                         Mus musculus clone
house mouse.
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ALTLTLPHMFGAPGAPSPLGWFAI"
a 897 c 703 g 498 t
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80.0%;
                                         RP23-69C19,
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Pred. No. 1.4e-80;
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                                         bp DNA
9, WORKING
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                                          DRAFT
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                                        linear HTG
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                                                                                                                                                                                                                                                 Consensus quality: 238523 bases at least Q40
Consensus quality: 246299 bases at least Q20
Consensus quality: 246299 bases at least Q20
Consensus quality: 247856 bases at least Q20
Estimated insert size: 25420; agarose-fp estimation
Estimated insert size: 24965; sum-of-contigs estimation
Quality coverage: 9.07 in Q20 bases; sum-of-contigs
expected insert size: 24965; sum-of-contigs estimation
Quality coverage: 9.07 in Q20 bases; sum-of-contigs

** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes

** of the gaps between them are based on estimates that have
** provided by the submittor.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** 34857 37541; contig of 34756 bp in length

** 34857 37541; contig of 34756 bp in length

** 37642 49922; contig of 12281 bp in length

** 37642 49923 contig of 12281 bp in length

** 97892 120188; contig of 27460 bp in length

** 120189 12889; contig of 2780 bp in length

** 120189 12889; contig of 2780 bp in length

** 120189 12889; contig of 2780 bp in length

** 120189 12889; contig of 2807 bp in length

** 12089 12889; contig of 2807 bp in length

** 13089 12892; gap of unknown length

** 150330 150429; gap of unknown length

** 160439 17823; contig of 2655 bp in length

** 160439 17823; contig of 2655 bp in length

** 171944 17408; contig of 2175 bp in length

** 171940 17408; contig of 2175 bp in length

** 171940 17409; contig of 5311 bp in length

** 1719510 179609; cantig of 5311 bp in length

** 1719510 179609; cantig of 5311 bp in length

** 1719510 179609; cantig of 5311 bp in length

** 1719510 179609; cantig of 5311 bp in length
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Center clone name: RPCI-23_69C19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 250615)
DDE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 250615)
DOE Joint Genome Institute.
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                           174099
174199
179510
179610
179610
185229
185329
190235
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190335
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191667
                           185228:
185328:
190234:
190334:
191566:
191666:
227834:
                                                                                                   contig of 5619 bp in 1 gap of unknown length contig of 4906 bp in 1 gap of unknown length contig of 1232 bp in 1
                                                 gap of contig
                                                                                                                                                                                                                gap of contig
f unknown length g of 36168 bp in f unknown length g of 16180 bp in
                                                                                                                                                                                                                                      f unknown
g of 5311
f unknown
                                                                                                                               bp in l
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length
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SOURCE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTTAACCGGAAAAATTGTCCTGGCTAGGAGGGAGGGAAGGACATGGCCCAGCTATCCT
                                          Direct Submission
Submitted (02-SEP-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                              unordered
AC079550
 Center
                Project Information
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 13418)
DOE Joint Genome Institute.
                                                                                                                                                         2 (bases 1 to 134189)
DOE Joint Genome Institute.
                                                                                                                                                                                                       Sequencing of Mouse
                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                 AC079550.1 GI:9964915
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                             AC079550

134189 bp DNA linear HTG
Mus musculus clone RP23-422A19, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                        Inpublished
                                                                                                                                                                                                                                                                                                    house mouse.
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244215
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Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-59C19"
/clone_lib="RPCI mouse BAC library
/ 61845 c 62764 g 62178 t 2004
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1. .250615
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98.7%;
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others
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NCE, 30
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94598, USA
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Consensus quality: 105629 bases at least Q40
Consensus quality: 11743 bases at least Q30
Consensus quality: 117545 bases at least Q20
Consensus quality: 117545 bases at least Q20
Estimated insert size: 208000; agarose-fp estimation
Estimated insert size: 131289; sum-of-contigs estimation
Quality coverage: 8.71 in Q20 bases; agarose-fp estimation
Quality coverage: 13.79 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
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Gu,Y.Z., Moran,S.M., Hogenesch,J.B., Wartman,L. and I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtcagcgcgcacctggacaaggcctccatcatgcgcctcacaatcagctacctgcgcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTGCTACCTGAAGGCCCTGGAGGGCTTCGTCATGGTGCTCACCGCCGAGGGAGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcctgctacctgaaggccctggagggtttcgtcatggtactcaccgccgagggagacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCGCCTCTGCGCCAGGGGAGTGGAACCAGGTGGGAGCAGGGGGAGAACCACTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCAGCCAGGAGACCGAGGTGCTGTACCAGCTGGCTCACACGCTGCCCTTCGCCCGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgcagccaggagacggaggtgctgtaccagctggcgcacactctgccctttgcgcgcggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGCAAGGTCGACCACGGAGCTGCGCAAGGAAAAGTCCCGGGATGCGGCCCGCAGCCGG
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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1708)

Isogai.T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Mishikawa,T., Nagai,K., Sato,H., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. an
                                                                                                                                                                                                                                                     NEDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo capping; fis (full insert sequence).
Homo sapiens embryo, 10 weeks whole embryo,
mRNA, clone_lib:HEMBA1 clone:HEMBA1000216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK021421 1708 bp
Homo sapiens cDNA FLJ11359 fis,
similar to HYPOXIA-INDUCIBLE FAC
                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                      Oshima,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                            Direct Submission
                                                                                                                                                                                          2 (bases 1 to 1708)
Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK021421.1 GI:10432600
                                                                                                                                                                                                                                                   human cDNA sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="rarsttelrkeksrdaarsrrsqetevlyqlahtlpfargvsah
LDKASIMRLTISYLRMHRLCAAGEWNQVGAGGEPLDACYLKALEGFVMVLTAEGDMAY
LSENVSKHLGLSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypoxia-inducible
/protein_id="AAC99397.1"
/db_xref="GI:4092037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -agcaggtggaaaaaggggggagagccactggac
                                                                                                                                                                                                                                                   project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265.4; DB 9
No. 7.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp mRNA linear is, clone HEMBA1000216, FACTOR 1 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
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University of Tokyo.

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                                                                                       ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                          724 atctgtgaagccatccccagctccccttccacga 758
                                                                                                                                                                                                                                                                                                                                                                                                                                     461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 CTGGAGCTCATTGGACACAGCATCTTTGATTTCATCCACCCCTGTGACCAAGAGGAGCTT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaagcggccacctggaaggtgctgcactgctcaggacatatgagggcctacaagccccct 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyccacttttccctycgaatgaagagcacgctcaccagcagagggggcacgctcaacctc
                                                                                                                                                                                                                                                                                                                                                                                gcacagacttcccctgccgggagccctcgctccgagcctcccctgcaatgcctggtgctt 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGTGCTTCTCCTTGCGCATGAAGAGTACGCTCACCAGCCGCGGGGCGCACCCTCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGACGCCCTGACCCCCAGCAGACCCTGTCCAGGAGGAAGGTGGAGGCCCCCCACGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGCGGCCACCTGGAAGGTGCTGAACTGCTCTGGACATATGAGGGGCCTACAAGCCACCT
                                                 Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                     Rattus norvegicus clone CH230-10B18, ***, 67 unordered pieces.
 Muzny,D.M.,
                                                                                                                       HTG; HTGS_PHASE1.
                                   Rattus.
                                                                                                     Norway
                                                                                                                                     AC095259.2 GI:17943467
                                                                                                                                                                                                          AC095259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                 (bases 1 to 167150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="146 bases segment is present in AK21653,
caused by alternative splicing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mrpaagaarrproctswitropspaasaptwtrplscaspsato ACTASAPQLELIGHSIFDFIHPCDQEELQDALTPQQTLSRKKVEAPTERCFSLRMKST LTSRGRTLNLKAATWKVLNCSGHMRAYKPPAQTSPAGSPDSEPPLQCLVLICEAIPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280^28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSLEPPLGRGAFLSRHSLDMKFTYCDDRVAEVAGYSPMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB13819.1"
/db_xref="GI:10432601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="HEMBA1000216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="compared to AK21653 and AC007193.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"cloning vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="embryo, 10 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.0%;
                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                       167150 bp
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*** SEQUENCING
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Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouke, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Bydd, N.C., Carron, F., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., David, R., Davis, C., Coyle, M.D., David, R., Davis, C., Coyle, M.D., David, R., Delgado, O., Davy-carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denny, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Delgado, O., Davy-carroll, R., Davis, C., Coyle, M., Carroll, R., Douthwalte, K.J., Davis, C., Coyle, M., Fally, S., Karthor, R., Garrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hernandez, J., Hornandez, J., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, S., Lihtarage, O., Lieu, C., Liu, J., Liu, W., Martin, R., Primus, E., Pull, L., Mohabat, K., Martin, R., Primus, E., Pull, L., M., Martin, R., Primus, E., Pull, L., M., Martin, R., Martin, R., Primus, E., Pull, L., M., Martin, R., Martin, R., Martin, R., Martin, 
          Unpublished
2 (bases 1
                                                                                                       Direct Submission
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(bases 1 to 167150)
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JOURNAL REFERENCE AUTHORS TITLE TITLE JOURNAL

Worley, K.C.

Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15625813. Direct Submission ----- Genome Center

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM

Center project name: GDPX

Assembly program: Phrap; version 0.990329First Center clone name: CH230-10B18

findPhrapList

Consensus quality: 128712 bases at least Q40 Consensus quality: 139536 bases at least Q30 Consensus quality: 148385 bases at least Q20 Estimated insert size: 136187; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 67 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951), Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, Institute of Technology Center Institute of Technology
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Algorithms and the sequence of the seq
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2 (bases I to 1841)
Isogai,T. and Otsuki,T.
Direct Submission
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Homo sapiens cDNA FLJ14033 fis, clone HEMBA1004479, weakly similar
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/translation="mrpaagaarproctswltropspaasaptwtrplscaspsatc
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ACTASAPQEELODALTPAGSPDSEPPLOCLVLICEAIPHPGSLEGFVWVLTAEGDMA
YLSENVSNHLGLSQLELIGHSIFDFIHPCDQEELQDALTPHLNTSSLLPKPQGTVSFL
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/tissue_type="whole embryo, mainly head"
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Mus musculus clone RP23-422A19,
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 105629 bases at least Q40 Consensus quality: 114783 bases at least Q30 Consensus quality: 117545 bases at least Q20 consensus quality: 117545 bases at least Q20 Estimated insert size: 208000; agarose-fp estimation Estimated insert size: 131289; sum-of-contigs estimation Quality coverage: 8,71 in Q20 bases; agarose-fp estimation Quality coverage: 13.79 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/organism="Mus musculus"
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Oncorhynchus
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PALAAFEPADSPCPASLLTKTVPQMDREISLRSLASQNAQRKRKMSLSQAVGIGGLLQ
DHPGPGKKLKVSELSHADAPFNRTILLLPTDLASRLLGISSEGSGSPFTLPQLTRYDC
EVNAPVGGRQLLLQGEELLSALDQVN*

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VPYLVLACDPIPHPSNIEAPLDTKTFLSRHTLDMKFTYCDERITELMGYDPEDLLNRS
VPYEYYHALDSDHLMKTHHNLFAKGQVSTGQYKHLAKRGGFVWFETQATVIYNKNSQP
QCVVCVNYVLSGIEEEKMMLSLEQTEDMRPVKKELEEESSEPEVSPULKEEKSPEL
DVIKLETRAVETQPLSSLDDKLEEPEALTLLAPAAGDTIISLDFSSPDSDILQKEVP
LYKDVMLPSTSDKLALPLSLLPPSDQHLVPNTSVDTTEVSTGPDSSSTPGSHSETEPD
SPLDFCFPMESDINAEFKLDMVETLFAINPEPKTPFTLQAMEDLDLEMLAPYIPMDDD
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MVLSEDGDMIYLSENVNKCLGLAQIDLTGLSVFEYTHPCDHEELREMLVHRTGTSKKS
KEPNTERSFFLRMKCTLTNRGRTVNVKSATWKVLHCSDHVRVHESPAEQIPGGHKEPS
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/protein_id="AAK30364.1"
/db_xref="GI:13561506"
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/db_xref="taxon:8022"
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0; Mismatches
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of Turku, Yliopistonmaki,
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М. Т.,
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                                                              ACCCCTCCAACATCGAGG
    agctccccttccacgatg 760
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Search completed: September Job time: 6900 sec 8, 2002, 07:29:17

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Mouse transcription Human protein seque Human protein seque Human protein seque Human protein seque HIF-lalpha variant A variant of human HIF-lalpha variant of human A variant of human
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Hypoxia-inducible	AAY94626	21	74	13.1	214	45
	AAB54411	21	99	13.6	222.5	44
	AAY52991	21	924	15.3	250.5	43
Drosophila melanog	ABB62764	22	958	15.3	251	42
Novel human diagno	ABG20868	22	828	16.1	264	41
Murine SIM (single	AAW30758	18	657	16.2	265	40
Ō	ABB71624	22	634		265	39
Novel human diagno	ABG28236	22	776		269	38
Human transcriptio	AAY06294	20	691	•	278.5	37
Drosophila melanog	ABB58562	22	1507	17.2	281	36
Mouse neuronal PAS	AAW68092	19	594	•	293.5	35
Human neuronal PAS	AAW68091	19	590	•	294	34
HIF-lalpha variant	AAY94635	21	756	•	323	ω
Novel human diagno	ABG20871	22	373	19.7	323	32
HIF-lalpha variant	AAY94630	21	613	•	345.5	31
Human protein se	AAB95649	22	237		426	30
Hypoxia inducible	AAW06558	18	805		444	29
HIF-1 alpha delta	AAW06559	18	373	•	444	28
Human endothelial	AAY79161	21	870	•	466	27
Human endothelial	AAW37097	19	870		466	26
Human endothelial	AAY79160	21	485		466	25
	AAY06290	20	870		467	24
Murine endothelia	AAW37098	19	875	29.2	477.5	23
Human lung tumour	AAB76854	22	826	•	495	22
Q,	AAY69407	21	826		495	21
Human hypoxia-ind	AAY94640	21	826	•	495	20
	AAY06289	20	826		495	19
	AAW80418	19	826	•	495	18
Human hypoxia indu	AAW06557	18	826		495	17
a va	AAY94636	21	813		495	16
of.	AAY84169	21	789	•	495	15
variant of	AAY84170	21	749	•	495	14
of.		21	724	30.3	495	13
A variant of human	AAY84172	21	710	30.3	495	12

ALIGNMENTS

RESULT AAY06295

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23-AUG-1999 (first entry)

Mouse transcription regulator MOP7.

AAY06295;

AAY06295 standard; Protein;

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Claim 6; Page 101; 106pp; English. WPI; 1999-371120/31. N-PSDB; AAX58986. MOP7; member of the PAS superfamily; bHLH-PAS; mouse; transcription regulator; hypoxia inducible factor 3 alpha Developmental signal transduction associated proteins Bradfield CA, Gu YZ, (WISC) WISCONSIN ALUMNI RES FOUND. 28-NOV-1997; 27-NOV-1998; 10-JUN-1999. W09928464-A2 Mus musculus 97US-0066863 98WO-US25314 Hogenesch JB,

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29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                            28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAPTERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLC------
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                             99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                            2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence SEQ ID NO:12422.
                                                                                                                                                                                                                                                                                                                                                                                                          detection;
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                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
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Pred. No. 7.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                       therapy;
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cc sequence and an oligonucleotide comprising a sequence complementary to a cc polynucleotide which comprises a 3'-end sequence, where the cc oligonucleotide which comprises a 3'-end sequence, where the cc oligonucleotide comprises at least 15 nucleotides, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and cc in gene therapy. The primers are useful for synthesising polynucleotides, cc particularly full-length cDNAs. The primers are also useful for the cc detection and/or diagnosis of the abnormality of the proteins encoded by ct full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and cc AAH3363 to AAH18742 represent human cDNA sequences; AAB92446 to captscent oligonucleotides, all of which are used in the exemplification co of the present invention.
                                                                                   RESULT
AAB94934
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Best Local S
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or an origonucreotice comprising a sequence complementary strand of a polynucleotide which comprises a 5'-end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising full-length cDNAs defined in the specification. Where a prime
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                                AAB94934;
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26-JUN-2001
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                                                                                                                                                            plqclvliceaip----hpgs 231
                                                                                                                                                                                                                                                         KLEAPTERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEP
                                                                                                                                                                                                                                                                                                                                QAPGPOSVDLCSSSLIHNPTPGTNFS-LELIGHSIFDFIHPCDQEELQDALTPRPNLSKK 168
                                                                                                                                                                                                  PLQCLVLICEAIPQLPFHDGA 249
                                                                                                                                                                                                                                      kveaptercfslrmkstltsrgrtlnlkaatwkvlncsghmraykppvqtspagspdsep
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, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 AA;
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(first entry)
                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.8%; Score 831; DB 22; 68.2%; Pred. No. 2.5e-77; tive 11; Mismatches 30;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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The present invention describes primer sets for synthesising 5602 Cf full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination complementary strand of a polynucleotide which comprises a 5'-end complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the coligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises a 1-east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, comparticularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13638 and CAAH3633 to AAH8742 represent human cDNA sequences; and AAH3629 to AAH3632 constant of the special seaf of the special sea
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Best Local S
Matches 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent oligonucleotides, of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-2000;
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02-MAY-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama
                                                                                                                                                                                                                                                                                                                               Conservative
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2000JP-0183767.
2000JP-0241899.
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99JP-0300253.
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T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                        35.0%;
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                                                                                                                                                                                                    -----ewnqvgaggepldacylkalegf
                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                         Score 573; DB 22;
Pred. No. 1.8e-50;
.1; Mismatches 27;
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                                                   CC full-length cloward defined in the specification. Where a primer set to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination companies and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 5'-end sequence complementary to a combination of the 5'-end sequence?3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and compensed in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the collars easily without any specialised methods. AAH013166 to AAH13632 and AAH13633 represent human anino acid sequences; AAB92446 to AAH3632 represent human cDNA sequences; AAB92446 to AAH3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                            represent oligonucleotides, all of the present invention.
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27-AUG-1999;
                                                                                                                                                                                                                                                                                                                  The present full-length
                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 13303; 2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                         and/or diagnosis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer
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                                        represented by the present sequence. The variants are useful for identifying compounds capable of modulating the function of a functional domain of human HIF-lalpha. The method comprises contacting a candidate compound with a cell expressing a HIF-lalpha variant conjugated to a molecular probe. The localization of the probe can be detected in the cell. The Aequeora victoria green fluorescent protein can be used as the molecular probe. The compounds are useful for the regulation of HIF-lalpha target genes, such as those involved in the regulation of
                                                                                                                                                                                                   This sequence represents a fragment of the hypoxia-inducible factor (HIF)-lalpha amino acid sequence. The mechanism of action of HIF-Lalpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-lalpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-lalpha between amino acids 173 and 390, a C-terminal nuclear localization sequence located at amino acids 718-584, a transactivator domain (N-TAD) located between amino acids 531 and 584, transactivator domain (N-TAD) located between amino acids 531 and 584, transactivator domain (N-TAD) located between amino acids 531 and 584,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypoxia-inducible factor lalpha; HIF-lalpha; PAS-B; N-TAD; regulation; angiogenesis; erythropoiesis; glycolysis; humar
                                                                                                                                                                          and a second transactivator domain (C-TAD) located between The invention relates to isolated variants of HIF-lalpha, s
                                                                                                                                                                                                                                                                                                                                                                                              Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIF-lalpha variant protein sequence HIF-lalpha/1-245
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                                                                                                                                                                                                                                                                                                                                                    13; Page 68-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 245
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Sequence

This sequence represents a fragment of the hypoxia-inducible factor (HIF)-lalpha amino acid sequence. The mechanism of action of HIF-lalpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-lalpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-lalpha between amino acids 173 and 390, a C-terminal nuclear localization sequence located at amino acids 718-584, a nuclear localization sequence located between amino acids 531 and 584, and a second transactivator domain (C-TAD) located between 813 and 826. The invention relates to isolated variants of HIF-lalpha, such as that represented by the research of the second variants of HIF-lalpha.

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Claim 15; angiogenesis,

Page 69-70;

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Best Local Similarity
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                                                                                                                                                        Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                       regulation; angiogenesis; erythropoiesis; glycolysis; human.
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Pred. No. 5.6e-43;
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                                                                                                                                                                                                                                                                                                            Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
 Claim
                         Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful treating hypoxia or ischemia-related tissue damage -
                                                                                                                                                                                                                                WO200010578-A1
                                                                                                                                                                                                                                                                                                                                                                  A variant of human hypoxia inducible factor-1 alpha protein.
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                                                                                                                                                 25-AUG-1998;
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                                                                                                                                                                                                     02-MAR-2000
                                                                                                                                                                                                                                                                        Synthetic.
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1; Page -; 96pp; English
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                                                                                                                        JOHNS HOPKINS SCHOOL MEDICINE
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Pred. No. 8.5e-43;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a variant of hypoxia-inducible factor (HIF)-1 alpha, comprising amino acids 1-391 and 576-826 of the wild type protein (see AA769407). The HIF-lalpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826, 512-826 or 517-826 of the wild type human HIF-lalpha polypeptide, in which residues 551 and 552 are not serine and threonine, respectively. The HIF-lalpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-lalpha polypeptides are useful for providing prophylactic therapy for inducing the level of and prophylactic therapy for inducing the level of and prophylactic for the provides and the level of and prophylactic therapy for inducing the level of and prophylactic for the provides and the level of and prophylactic for the provides and the level of and prophylactic for the provides are useful for providing prophylactic therapy for inducing the level of and prophylactic for the provides are useful for providing prophylactic therapy for inducing the level of and prophylactic for the provides are useful for providing prophylactic therapy for inducing the level of and prophylactic for the provides are useful for providing prophylactic therapy for inducing the level of and prophylactic for the provides are useful for providing prophylactic therapy for inducing the level of and prophylactic therapy for inducing the level of the provides are useful for providing prophylactic therapy for inducing the level of the provides are useful for provides are useful for provides and prophylactic therapy for inducing the prophylactic prophylactic therapy for inducing the prophylactic prophylactic prophylactic prophylactic prophylactic prophyla
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                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                          regulation; angiogenesis;
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46.2%;
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Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear localization sequence located at amino acids 718-584, a transactivator domain (N-TAD) located between amino acids 531 and 584, and a second transactivator domain (C-TAD) located between 813 and 826. The invention relates to isolated variants of HIF-lalpha, such as that represented by the present sequence. The variants are useful for identifying compounds capable of modulating the function of a functional domain of human HIF-lalpha. The method comprises contacting a candidate compound with a cell expressing a HIF-lalpha variant conjugated to a molecular probe. The localization of the probe can be detected in the cell. The Aequeorar victoria green fluorescent protein can be used as the milecular probe. The compounds are useful for the regulation of antiquence is certificated as those involved in the regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a fragment of the hypoxia-inducible factor (HIF)-lalpha amino acid sequence. The mechanism of action of HIF-lalpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-lalpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-lalpha between amino acids 173 and 390, a C-terminal
                              Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery diseasischemic tissue damage.
                                                                                                                         A variant of
                                                                                                                                                                                                                                       AAY84167 standard; Protein; 669
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                                                                                                                                                                03-JUL-2000
                                                                                                                                                                                                      AAY84167;
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Pred. No. 2.3e-42;
6; Mismatches 59;
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AAY84166

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AAY84166 standard;

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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page -; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating hypoxia or ischemia-related tissue damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200010578-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note: this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-AUG-1999;
222
                                                                  164
                                                                                                    175
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                                                                                                                                                                         121
                                235 LICEAIP 241
                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                          71 AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC 120
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
licepip
                                                                                                                                                   SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174
                                                                  qrsfflrmkctltsrgrtmniksatwkvlhctghihvydtnsnqpqcg--ykkppmtclv
                                                                                                   ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV 234
                                                                                                                                   dgdmiyisdnvnkymgltqf.-eltghsvfdfthpcdheemremlthrnglvkkgkeqnt 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-246493/21
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                                                                                                                                                                                                                                                                                                                                              Conservative
228
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                                                                                  98US-0148547
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                                                                                                                                                                                                                                                                                                                                                               30.3%;
                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                             Score 495; DB 21;
Pred. No. 2.4e-42;
                                                                                                                                                                                                       ----dldieddmkaqmncfylkaldgfvmvltd 105
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                             Length 669;
                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                   Matches
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ischemic
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                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                     or ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A variant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating
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   121
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                                                                                                     NTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
 SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-246493/21
                                                         AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA---
                                                                                      sserrkeksrdaarsrrskesevfyelahqlplphnvsshldkasvmrltisylrvrkll 73
                                                                                                                                                   114;
                                                                                                                                                                                                                                                       information
                                                                                                                                                                                                                                                                        this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forms of hypoxia-inducible factor (HIF)-1 alpha, g hypoxia or ischemia-related tissue damage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related damage; angiogenesis; coronary artery disease;
tissue damage.
                                                                                                                                                                                                                           697
                                                                                                                                                   Conservative
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                                                                                                                                                30.3%; Score 495; DB 21;
46.2%; Pred. No. 2.5e-42;
Live 26; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "this residue is optionally not Thr, preferably Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "this residue is preferably Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inducible factor-1 alpha
                             -dldieddmkaqmncfylkaldgfvmvltd 105
                                                                                                                                                                                                                                                                     the specification; it was created
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                                                                                                                                                   59;
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                                                         -----PGPQSVDLC 120
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RESULT
AAY84173
                                     The present sequence represents a variant of hypoxia-inducible factor (HIF)-l alpha, comprising amino acids 1-91 and 517-826 of the wild type protein (see ANK69407). The HIF-lalpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 499-826, 578-826 or 517-826 of the wild type human HIF-lalpha ocid polypeptide, in which residues 551 and 552 are not serine and threonine, respectively. The HIF-lalpha variant polypucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-lalpha polypeptides are useful for providing prophylactic therapy for inducing the level of angiogenesis in tissues of patients at risk of coronary artery disease
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                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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                           ischemic tissue damage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             licepip
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       A variant of human hypoxia inducible factor-1 alpha protein.
         Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for treating hypoxia or ischemia-related tissue damage -
                                       WPI; 2000-246493/21
                                                                                                                                                                                                                                                                                    Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage.
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                                                                                                 25-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dag-----ylkaldgfvmv1td 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114;
                                                           GL;
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                 98US-0148547
                                                                                                                    99WO-US19416
                                                                                                                                                                                                   436
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                         /note=
                                                                              HOPKINS SCHOOL MEDICINE
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                                                                                                                                                                             "this residue is not Thr, preferably Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 495; DB 21;
Pred. No. 2.5e-42;
6; Mismatches 59;
                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 701;
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AAY84171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC (HFF)-1 alpha, comprising amino acids 1-391 and 508-826 of the wild CC (type protein (see AAY69407). The HIF-lalpha variants are stable under CC hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 512-826 or 517-826 of the wild type human HIF-lalpha CC 508-826, 512-826 or 517-826 of the wild type human HIF-lalpha CC polypeptide, in which residues 551 and 552 are not serine and threonine, CC respectively. The HIF-lalpha variant polynucleotide sequences are useful CC for increasing expression of a hypoxia inducible gene in a cell. They cis also useful for providing constitutive expression of a hypoxia or cischemia related damage. The variant HIF-lalpha polypeptides are useful for providing prophylactic therapy for inducing the level of angiogenesis in tissues of patients at risk of coronary artery disease or ischemic tissue damage.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                             Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia;
                                                                                                                                                                                                                                        A variant of human hypoxia inducible factor-1 alpha protein.
                              Misc-difference
                                                                                                                                    Synthetic
                                                                                                                                                                               hypoxia inducible gene; hypoxia induci
ischemia related damage; angiogenesis;
                                                                                                                                                                                                                                                                      03-JUL-2000
                                                                                                                                                                                                                                                                                                  AAY84171;
                                                                                                                                                                                                                                                                                                                               AAY84171 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page -; 96pp;
                                                                          Misc-difference
                                                                                                                     Homo sapiens
                                                                                                                                                                 ischemic tissue
                                                                                                                                                                                                                                                                                                                                                                                                   222 licepip 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sserrkeksrdaarsrrskesevfyelahqlplphnvsshldkasvmrltisylrvrkll 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dgdmiyisdnvnkymgltqf--eltghsvfdfthpcdheemremlthrnglvkkgkeqnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                     (first entry)
                              450
                                                                         Location/Qualifiers 449
                                                                                                                                                                damage.
                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.3%;
"this residue is
preferably Ala"
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                                                           "this residue is
                                          preferably Gly"
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                                                                                                                                                                                                                                                                                                                                724 AA.
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Pred. No. 2.6e-42;
6; Mismatches 59;
                                                                                                                                                                                 coronary artery disease
               not Thr,
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                and
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RESULT 1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note: this sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variant forms of hypoxia-inducible factor (HIF)-1 alpha, treating hypoxia or ischemia-related tissue damage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-246493/21
   03-JUL-2000
                               AAY84170;
                                                          AAY84170 standard; Protein; 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                                         LICEAIP 241
                                                                                                                                                                                                                                                           SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPPRPNLSKKKLEAPT
                                                                                                                              licepip
                                                                                                                                                                                    qrsfflrmkctltsrgrtmniksatwkvlhctghihvydtnsnqpqcg--ykkppmtclv
                                                                                                                                                                                                                                            dgdmiyisdnvnkymgltqf--eltghsvfdfthpcdheemremlthrnglvkkgkeqnt 163
                                                                                                                                                                                                     dag-----dldieddmkaqmncfylkaldgfvmvltd
                                                                                                                                                                                                                                                                                                                                 AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
 (first entry)
                                                                                                                                 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9805-0148547
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                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 495; DB 21;
Pred. No. 2.7e-42;
6; Mismatches 59
                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                         59;
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Matches 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-Lalpha polypeptides are useful for providing prophylactic therapy for inducing the level of angiogenesis in tissues of patients at risk of coronary artery disease or ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Semenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rey
Location/Qualifiers
Misc-difference 474
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                using information provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respectively. The HIF-lalpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They for increasing expression of a hypoxia constitution of a hypoxia or increasing the constitution of a hypoxia or increasing the constitution of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; hypoxia-inducible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
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SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174
                                                                                                                                                                              sserrkeksrdaarsrrskesevfyelahqlplphnvsshldkasvmrltisylrvrkll 73
                                                                                                                                                                                                         sapiens.
                                                                                                                                AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this sequence
                                                                                                                                                                                                                                                                                    Similarity 46.2
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page -; 96pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypoxia or
                                                                                                                                                                                                                                                                                                                                                                                                                  749 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US19416
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                                                                                                                                                                                                                                                                                                       30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ischemia-related tissue
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preferably Ala"
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preferably Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e factor 1 alpha; HIF-lalpha; var
hypoxia inducible factor; hypoxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not appear in
                                                                                                                                                                                                                                                                                  ; Score 495; DB 21;
; Pred. No. 2.8e-42;
26; Mismatches 59
                                                                             --dldieddmkaqmncfylkaldgfvmvltd 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the specification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not Thr,
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                                                                                                                                                                                                                                                                                                                                  Length 749;
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                                                                                                                                -----PGPQSVDLC 120
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RESULT 1
                                          The present sequence represents a variant of hypoxia-inducible factor (HIF)-1 alpha, comprising amino acids 1-31 and 429-826 of the wild type protein (see AAY69407). The HIF-1alpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 498-826, 494-826, 508-826, 512-826 or 517-826 of the wild type human HIF-1alpha polypeptide, in which residues 551 and 552 are not serine and threonine, respectively. The HIF-1alpha variant polypucleotide sequences are useful for increasing expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-1alpha polypeptides are useful for providing prophylactic therapy for inducing the level of angiogenesis in tissues of patients at risk of coronary artery disease
        note:
                          angiogenesis
or ischemic t
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page -; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful treating hypoxia or ischemia-related tissue damage -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A variant of human hypoxia inducible factor-1 alpha protein.
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Pred. No. 3e-42;
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protein -9

Perfect score:

Scoring table: Sequence:

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38, Appl 38, Appl 16, Appl 47, Appl 47, Appl 47, Appl 47, Appl 47, Appl 51, Appl 51, Appl 51, Appl 53, Appl 55, Appl

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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Gapop 10.0 , Gapext 0.5
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US-08-785-241-6
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US-08-15-213-2
US-09-148-547-2
US-09-148-547-2
US-09-235-241-7
US-08-785-241-7
US-08-785-241-7
US-08-785-241-7
US-08-915-213-3
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US-08-915-213-4
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US-08-915-213-36
US-08-785-310A-5
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                                                                                                                                                             TENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-241-6
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PCFE4
COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,241
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 6:
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US-08-785-241-6
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                                                                      Query Match
Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Endothelial PAS Domain I
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McKnight, Steve
APPLICANT: Russell, David
APPLICANT: Tian, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
ZIP: 941
14 SSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLL 73
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US-08-971-188-10
US-08-971-188-8
US-08-971-188-8
US-08-971-188-7
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US-08-915-213-47
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US-08-915-213-47
US-08-971-188-12
US-08-971-188-5
US-08-971-188-7
                                                                      Score 495; DB 1;
Pred. No. 1.1e-45;
26; Mismatches 59
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Result No.

Score

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS PC-DOS/MS-DOS
COERNATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 TYPE: amino acid
106
              235 LICEAIP 241
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CITY: I
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                                                                                         71 AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC 120
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                                                                                                                                       FILING DATE: 06 CLASSIFICATION:
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DGDMIYISDNVNKYMGLTQF--ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNT 163
                                                                                                                       SSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLL 73
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                                                                                                                                                                                                                                                                                                                      826 amino acids
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N: 514
                                                                                                                                                                                30.3%; Score 495; DB 2; Length 826; 46.2%; Pred. No. 1.1e-45; rative 26; Mismatches 59; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/480 FILING DATE: 06-UN-1995 ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
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PRIOR APPLICATION DATA:
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             175 ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV 234
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                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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QRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCG--YKKPPMTCLV
                                                                          SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174
                                                         DGDMIYISDNVNKYMGLTQF--ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNT 163
                                                                                                                                              AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC 120
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                                                                                                                                                                                                                                   h 30.3%; Score 495; DB 3; Similarity 46.2%; Pred. No. 1.1e-45; 14; Conservative 26; Mismatches 59;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 826
TYPE: PRT
ORGANISM: Homo sapiens
US-09-148-547-2
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US-09-148-547-2
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APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: Hypoxia Inducible Factor-1 and I
FILE REFERENCE: 07265/151001
CURRENT APPLICATION NUMBER: US/09/148,547
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/235,217
FILING DATE:
                                                                                                                                                                                                                                                                            APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1
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CORRESPONDENCE ADDRESS
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
APPLICANT: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acid
                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10251
FILING DATE: 06-JUN-1996
                               ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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NAME: Haile, Lisa A.
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TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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CITY: La
STATE: CA
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                                                                                                      CLASSIFICATION:
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46.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 495; DB 4; I; Pred. No. 1.1e-45; 26; Mismatches 59;
                                  07265/053WO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07265/053001
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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INFORMATION FOR SEQ ID NO:
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSE
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
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                                                                   TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 826 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Russell, I
APPLICANT: Tian, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Endothelial PAS Domain Protein NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STRANDEDNESS:
                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                               APPLICATION NUMBER: US/C
FILING DATE: 17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC 120
                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LICEPIP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCG--YKKPPMTCLV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAG-----DLDIEDDMKAQMNCFYLKALDGFVMVLTD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7, Application US/08785241
5. 5695963
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                amino acid
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                              810 amino acids
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Russell, David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven L.
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                                                                                                                                          UTSD:1229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
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; MOLECULE TYPE: US-08-785-241-5
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Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                  TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McKnight
APPLICANT: Russell,
APPLICANT: Tian, Hu
                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208
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                                                                                                                                                                                                                      FILING DATE: 17-JAN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                       94104
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                                                                                                                                                                                                                                                                                                                                                                                    CALIFORNIA
                                                                     875 amino acids
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SYSTEM: PC-DOS/MS-DOS
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                            linear
                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                   US/08/785,241
                                                                                                                                                                          36,627
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                                                                                                                                                            UTSD:1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 489; DB 1;
Pred. No. 4.8e-45;
7; Mismatches 59
                                                                                                                                                                                                                                                                                 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                         ; MOLECULE TYPE: US-08-785-241-4
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Best Local Similarity
                                                                   Matches 111;
                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 343-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING .... 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
NAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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1 MALGLQRVRSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISYLRMHRL----CAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQS 116
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Russell, David W.
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                                                                   Conservative
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Pred. No. 1e-43;
3; Mismatches 79;
                                                               Score 466; DB 1;
Pred. No. 1.8e-42;
4; Mismatches 82;
                                                                                                                        Length 870;
                                                               Indels
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US-08-480-473B-3
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Best Local Similarity
Matches 104; Conserv
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STREET: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-JU CLASSIFICATION: 51
 56
                            83 LLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLCSSSLIH-----N 127
                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ISYLRMHRL----CAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDLCSSSLIHNPTPGTNFSLELIGHSIFDFIHPCDQEELQDALTPR--PNLSKKKLEAPT 174
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                                                                                                                                 27.18;
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-DLDIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVN
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                                                                                                                     Score 444; DB 2; 1
Pred. No. 1.4e-40;
Pred. Mismatches 59;
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                                                                                                                                                 Length 373;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
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155
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Local Similarity 44.3%; Pr
les 104; Conservative 24;
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             TSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLICEAIP 241
                                                                     PTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPTERHFSLRMKSTL 186
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                                                       KYMGLTQF--ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNTQRSFFLRMKCTL
                                                                                                                                                                      AGSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDAG------
                                                                                                                                        LLPEGPGGFRHGTHRRGRHGLPVGKCQQA------PGPQSVDLCSSSLIH-----N 127
TSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCG--YKKPPMTCLVLICEPIP
                                                                                                              ------DLDIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVN
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Lisa A.
THRER: 38,347
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Pred. No. 1.4e-40;
4; Mismatches 59;
                                                                                                                                                                                                                                                        DB 3; Length 373;
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207
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; MOLECULE TYPE:
US-09-235-217-3
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US-09-235-217-3
Sequence 3, Application PC/TUS9610251
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD (
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09235217 Patent No. 6222018
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Semenz
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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44.38;
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HYPOXIA INDUCIBLE FACTOR-1 AND
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Pred. No. 1.4e-40;
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                        AND METHOD OF USE
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

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Fish & Richa 5 Executive

& Richardson P.

Square,

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US-08-480-473B-4
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INFORMATION FOR SEQ ID NO: 3:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                               APPLICANT: Semenza, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: not
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   STATE:
                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, St
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IBM PC compatible
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HYPOXIA INDUCIBLE FACTOR-1
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Best Local Similarity
Matches 104; Conserv
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
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CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,473
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
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ZIP: 92037
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                                                                                         CLASSIFICATION:
                                                                                                    APPLICATION NUMBER: FILING DATE: 20-AUC
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                                                                                                 NUMBER: US/08/915,213
20-AUG-1997
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44.3%; Pred. No. 4.4e-40;
                                                                                                                                                        Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: 07265/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-213-4
Search completed: September Job time: 2907 sec
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                                                                   56 ------DLDIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVN 96
                                                                                                                                                                                                               83 LLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLCSSSLIH-----N 127
             8
            2002, 07:33:59
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                    6;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                      Database :
                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                  September 8, 2002, 07:32:32; Search time 37.72 Seconds (without alignments) 782.063 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                 US-09-896-791B-3
1636
1 MALGLQRVRSNTELRKEKSR.....TESSLPSWVLWALNRKNCPG 307
                                                                                                                                                                                                                                                            283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
pir1:*
pir2:*
pir3:*
pir4:*
                                                                                                                                                                                                                              283138
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	w	2	_	NO.	Result
86	102	102.5	103	103	103.5	104.5	106	123.5	125.5	128	129	129.5	129.5	136.5	136.5	138.5	138.5	142	169.5	169.5	202	256	281	485	492	495	503	802	score	
6.0	6.2	•	6.3		6.3	6.4	6.5	7.5	7.7	7.8	7.9	7.9	7.9	8.3	8.3	8.5	8.5	8.7	10.4	10.4	12.3	15.6	17.2	29.6	30.1	30.3	30.7	49.0	Match	Query
850T	716	271	1079	846	258	1059	848	626	626	56	453	451	358	789	776	791	392	805	825	823	655	248	1505	813	810	826	811	667	Length	:
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T30556	T09462	PC4288	A70972	JC7721	JC5407	T30557	S59514	JE0270	JC5405	A41647	T19440	T42397	S58376	I59550	A55448	A56241	JC7633	JC7635	T21944	T21943	A29945	A58520	JC4851	JC5809	JC4837	138972	JC7619	JC7771	T T	
aryl hydrocarbon r	juvenile hormone r	brain and muscle A	probable DNA polym	aryl hydrocarbon r	=		aryl hydrocarbon r	Arnt-like PAS prot	brain and muscle A	neurogenesis regul	4	hydrocarbon		aryl hydrocarbon r	Ah receptor nuclea			aryl hydrocarbon r	hypothetical prote		neurogenesis regul	single-minded gene	hypoxia-inducible	hypoxia-inducible	hypoxia-inducible	hypoxia-inducible	1	xia inducibl	Description	

RESULT 2
JC7619
hypoxla-inducible factor 1 alpha - chicken
C;Species: Gallus gallus (chicken)

			•	
0	Qu Be Ma Qy Db	RESULT hypoxi- C:Spec C:Spec C:Date C:Date C:Date R:Hara Bioche R:Titl A:Refal A:Cont A:Ace A:Cont Cont Cont Cont A:Gene		
118 107 177 161 237 221	Query Matc Best Local Matches 1 9 RS 7 RS y 69 LC y 69 LC y 67 LC	SULT 1 7771 Species: I Species: I Date: Ol-1 Accession Hara, S.; ochem. Bi Title: Exy Reference Contents: Accession		33333333333333333333333333333333333333
DLCSSSLIHNPTP		a inducible ; lies: Homo sa; : 01-Feb-200; ssion: JC777; ss. Hamada m. Biophys. le e Expression rence number ents: Kidney seiche type: midues: 1-667; sreferences ent: This pronther regulatics: hif-3alpha: hif-3		97.5 97.5 94.5 94.5 93.5 99.5 90.5 90.5 87.5 87.5
DLCSSSLIHNPTPGTNF	Similarity 72; Conserva 11:	fact jien 2 #s 2 #s 1 J . 1 an 1 an 1 J . 1 J .		@ @ @ @ @ @ C F W W W & 4 & & & & & & & & & & & & & & &
TNFS-L 	49.0% 68.0% ative arsersol	ctor-3 alpha ens (man) #sequence_rev J.; Kobayashi s. Commun. 28 and character JC7771; PMID: A AR DDBJ:AB054067 DDBJ:AB054067 DDBJ:AB054067 DDBJ:AB054067		326 527 920 300 1151 1751 1751 743 1920 1891 1891 1893 3133 3133 3133 1920 1893
ELI ELI AAT	%; %; QET QET QET	ha rev shi 28 ter ID: 067		00000000000000000
GHSIFDF	Score Pred. 1; Mis EVLYQLA EVLYQLA EVLYQLA EVLYQLA EVLYQLA EVLYQLA	- hume ision , C.; 7, 808 izatic izatic 115739	ALIG	\$71755 JC73199 JC73199 JC73193 T24292 T09354 T09394 T09394 G83726 G83726 G83726 G83726 G83726 G83726 G83726 G83726 G83726
LCSSSLIHNPTPGTNFS-LELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPTERLSENVSKHLGLSQLELIGHSIFDFIHPCDQEELQDALTPQCTLSRRVEAPPTER FSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLI	tch 49.0%; Score 802; DB 2; Length 667; al Similarity 68.0%; Pred. No. 7.4e-62; 172; Conservative 11; Mismatches 28; Indels 42; Grsntelrkeksrdaarsrrsgetevlyglahtlpfargvsahldkasimrltisylrmhr [-2002 #text_ Y.; Imura, 2001 ypoxia-induc ypoxia-induc	ALIGNMENTS	
NLSKKLEA	Hh 667; Hels 42; HILLISYLRM HILLISYLRM HILLISYLRM QAPGPQ FVMVLTAEGDM	ange O le fac le fac		transcription fact hypothetical prote aryl hydrocarbon re hypothetical prote hypothetical prote hypothetical prote gag-pro-pol polypr assimilatory nitra gene hindsight pro hypothetical prote hypothetical prote hypothetical prote aryl hydrocarbon re silkwo steroid hormone re aryl hydrocarbon re fibronectin - Afri hypothetical prote
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	5;	3alpha		wrnwondowndundr
		na in		
		σ ^π		

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C;Genetics:
A;Gene: GDB:HIF1A
A;Cross-references: GDB:512229
A;Map position: 14q21-14q24
                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-826 <RESS
A; Residues: 1-826 <RESS
A; Cross references: EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g881346
A; Note: parts of this sequence were confirmed by peptide sequencing
R; Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.
submitted to the EMBL Data Library, June 1995
A; Reference number: H00692
A; Accession: G01875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypoxia-inducible factor 1 alpha - human
N;Alternate names: ARNT interacting protein
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 05-Nov-1999
C;Accession: I38972; G01875
R;Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995
A;Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulate
A;Reference number: I38972; MUID:95296340
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: hif-lalpha
C;Keywords: embryo; transcription factor
F;106-156/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS1>
F;249-299/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS2>
F;262-811/Domain: conserved carboxy-terminal transactivation element #status predicted <F;767-768/Region: conserved dileucine repeat, important for oxygen-dependent degradation
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C;Accession: JC7619
R;Takahashi, T.; Sugishita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kinugawa, K.; Harada, Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001
Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001
A;Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventricu. A;Reference number: JC7619; MUID:21134360; PMID:11237772
A;Contents: Embryonic ventricular myocytes
A;Accession: JC7619
                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-826 <HOG>
A;Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-811 <7DAY
A; Cross-references: DDBJ: AB013746
C; Comment: This factor belongs to the basic
eostasis of cells, and in redox stimuli.
C; Genetics:
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Keywords:
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLICEAIP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIHNPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPTERHFSLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLDAGELETEANMEKELNCFYLKALDGFVMVLSEDG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCTLTSRGRTVNIKSATWKVLHCTGHIRVYDTCNNQTHCG--YKKPPMTCLVLICEPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENVNKCMGLTQF--DLTGHSVFDFTHPCDHEELREMLTHRNGPVKKGKEQNTERSFFLRM 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHR 68
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nilarity 49.8%;
Conservative 2
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Pred. No. 1e-35;
0; Mismatches
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                                                                                                                                       PID:g1144013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DMIYMS 113
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Query Match 30.3%; Score 495; DB 2; Length 826; Best Local Similarity 46.2%; Pred. No. 5.2e-35; Matches 114; Conservative 26; Mismatches 59; Indels 48; Gaps 6	<u></u> '
QY 11 NTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLC 70 ::	
QY 71 AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLC 120	
QY 121 SSSLIHNPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174	
Qy 175 ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV 234 :	
Qy 235 LICEAIP 241 Db 222 LICEPIP 228	
RESULT JC4837 JC4837 JC4837 Approxia-inducible factor 1 alpha - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Ju1-2000 C;Accession: JC4837 R;Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M. Biochem. Biophys. Res. Commun. 223, 54-59, 1996 A;Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mc A;Reference number: JC4837 A;Reference number: JC4837; MUID:96254028 A;Accession: JC4837 A;Molecule type: mRNA A;Residues: 1-810 <wenna 1-810="" <wenna="" a;residues:="" factor="" in="" involved="" is="" of="" oxygen-regulated="" se<="" td="" the="" this="" transcription=""><td>mouse hyp</td></wenna>	mouse hyp
A;Gelne: Hilalpha A;Map position: 12 C;Keywords: transcription factor F;5-58/Region: helix-loop-helix #status predicted F;5-58/Region: helix-loop-helix #status predicted Query Match Query Match Best Local Similarity 45.0%; Pred. No. 9.3e-35; Best Local Similarity 45.0%; Pred. No. 9.3e-35; Matches 112; Conservative 26; Mismatches 59; Indels 52; Gaps 5	Ţ.
Qy 11 NTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLC 70 ::	
Qy 71 AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPG 113	
Qy 114 PQSVDLCSSSLIHNPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEA 172	
Qy 173 PTERHESLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSBRSEPDLQC 232 :	
Qy 233 LVLICEAIP 241 	

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C:Species: Drosophila melanogaster
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #te
C:Accession: JC4831
R:Nambu, J.R.; Chen, W.; Hu, S.; Crews, S.T.
Gene 172, 249-254, 1996
A;Title: The Drosophila melanogaster similar bHLH-PAS
A;Reference number: JC4851; MUID:96269413
A;Accession: JC4851
A;Molecule type: mRNA
A;Residues: 1-1505 <NAM>
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C.Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999
C.Accession: JC5809
R.Ladoux, A.; Frelin, C.
Blochem. Blophys. Res. Commun. 240, 552-556, 1997
Blochem. Blophys. Res. Commun. 240, 552-556, 1997
A;Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop hellows the community of th
                                                                                                                                                                                                                        A;Map position: 3
F;72-125/Region: helix-loop-helix #status predicted
F:171-433/Region: PAS domain #status predicted
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C;Comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, especially. F;6-144/Region: basic helix-loop-helix #status predicted
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F;506-635/Region:
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                                                                                                                                                                                                                                                                                                                                                                             A;Gene: sima
                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U43090; NID:g1174073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypoxia-inducible factor 1 alpha homolog - fruit fly (Drosophila melanogaster)
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Matches 112; Conserv
                                                                   Matches
                                                                                                Query Match
Best Local
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                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLC
RSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LICEPIP
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                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
                                                                                                                                                                                                                     proline-rich
                                                                                          17.2%;
30.2%;
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                                                                47;
                                                             Score 281; DB
Pred. No. 4.6e
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 485; DB
Pred. No. 3.8e
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ····---DLDIEDEMKAQMNCFYLKALDGFVMVLTD
                                                             DB 2; I
4.6e-16;
hes 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAC47303.1; PID:g1174074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHLH-PAS
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.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 21-Jul-2000
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                                                                                                                       Length 1505;
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                                                                Indels
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RGRATGRLLPEGPGGFRHGTHRRGRHGLPV--

-GKCQQAPGPQSVDLCSSSL 124

2 KEKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEG--

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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change
C;Accession: AS8520; ITS111; I78524; I78523; S61256
R;Oscegawa, K.; Okano, S.; Kato, Y.; Nishimura, Y.; Soeda, E.
DNA Res. 3, 175-179, 1996
A;Tille: A 19-kb CGG island associated with single-minded gene 2
A;Reference number: A58520; MUID:97061206
               Q
                                                                                                                                                                    A;Gene: hSIM2
F;1-50/Region:
                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 87-116 <D
                                                                                                                                                                                                                                                                                                                                      A;Description: Down syndrome critical region A;Reference number: S61256
                                                                                                                                                                                                                                                                                                                                                                                 R;Delabar, J.M.; Dahmane, X.Y.Z. submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 87-116 <RE3>
A;Cross-references: GB:D44445; NID:g1088452; PIDN:BAA07907.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 117-152 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references:
A;Accession: 178524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I58111
A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Chen, H.; Chrast, R.; Rossier, C.; Gos,
Nature Genet. 10, 9-10, 1995
A;Title: Single-minded and Down syndrome?
A;Reference number: 158111; MUID:95375794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: A58520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single-minded gene 2 protein - human (fragment)
C;Species: Homo saniana /mar\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                A;Cross-references: EMBL:X84790; NID:g971469; PIDN:CAA59261.1; PID:g971470
                                                                                                                                                                                                                                                                                                                       A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: 178523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-58 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
A; Residues: 1-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:D85922
                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                 Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 RELAQKVKDEPQQNSGVSTHHRDLFVRLKCTLTSRGRSINIKSASYKVIHITGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 MLQFVPSLRDCNDDIKQDIETAE------DQQEVKPKLEVGTEDWLNGAEAREL
16 KEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGGK 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKQTMDGFLLVLSHEGDITYVSENVVEYLGITKIDTLGQQIWEYSHQCDHAEIKEALSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRNNEKRKEKSRDAARCRRSKETEIFMELSAALPLKTDDVNQLDKASVMRITIAFLKIRE
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                                                                                Similarity
                                                                                                                                                                    helix-loop-helix #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:D44444; NID:g1088450; PIDN:BAA07906.1;
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                                                                                    35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHM
                                                                26;
                                                            Score 256; DB 2;
Pred. No. 8.3e-15;
6; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.; Yamaki,
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chr

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neurogenesis regulatory protein - fruit fly (Drosophila N;Alternate names: single-minded gene protein C;Species: Drosophila melanogaster C;Date: 15-Dec-1988 *sequence_revision 15-Dec-1988 *text.C;Accession: A29945 *Thomas, J.B.; Goodman, C.S. R;Crews, S.T.; Thomas, J.B.; Goodman, C.S. Cell 52, 143-151, 1988 *A;Reference number: A29945; MUID:88151023 *A;Accession: A29945                                                     A; Molecule type: DNA
A; Residues: 1-823 <WIL>
                                                                                                                                        A; Reference number: A; Accession: T21943
                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19491
                                                                                                                                                                                                                                                               hypothetical protein F38A6.3a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *te. C;Accession: T21943; T26899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
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A; Experimental source:
                            A; Cross-references:
                                                                                                            A; Status: preliminary; translated from
                                                                                                                                                                                                                                         R; Mortimore,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M19020; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-655 <CRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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73; Conservative
EMBL:Z92833; PIDN:CAB07380.1; GSPDB:GN00023; ce: clone F38A6
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A;Accession: T2689
A;Status: preliminary; translated
A;Molecule type: DNA
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A; Introns: 19/2;
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A; Map position: 5
A; Introns: 19/2; 75/1
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A; Cross-references: EMBL:ALO:
A; Experimental source: clone
C; Genetics:
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A; Map position: 5
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A;Experimental source: clone Y44A6D
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A; Residues: 1-825 <WI2>
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A;Cross-references: EMBL:Z92833; PIDN:CAB07381.1; GSPDB:GN00023; CESP:F38A6.
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                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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ce: clone Y44A6D
                                                                                                                                                                                                                                       111/2; 175/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%;
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                                                                                    35;
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                                                                                                                Score
Pred.
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Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAA19521.1;
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                                                                                    Mismatches
                                                                                                                                                                                                                                       226/3;
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                                                                                                                169.5; DB 2
No. 1.2e-06;
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                                                                                    Indels
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aryl hydrocarbon nuclear translocator ARNT2-like factor, C;Species: Brachydanio rerio (zebra fish)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_C;Accession: JC7633
R;Hsu, H.J.; Wang, W.D.; Hu, C.H.
Blochem. Biophys. Res. Commun. 282, 487-492, 2001
A;Title: Ectopic expression of negative ARNT2 factor disr
A;Reference number: JC7633; MUID:21294759; PMID:11401485
A;Contents: Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-805 < CAT>
C; Comment: This protein, known as hypoxia-inducible ponses to hormonal and environmental stimuli. It is C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aryl hydrocarbon receptor nuclear translocator 1 - chicken N;Alternate names: hypoxia-inducible factor 1 beta C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_chan C:Accession: JC7635
R:Catron, T:, Mendiola, M.A.; Smith, S.M.; Born, J.; Walker, Biochem. Biophys. Res. Commun. 282, 602-607, 2001
A:Title: Hypoxia regulates avian cardiac Arnt and HIF-lalpha A:Reference number: JC7635; MUID:21294777; PMID:11401503
A:Contents: Embryo
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JC7633
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C;Keywords: transcription
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Best Local
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                                                                                                                                                                                                                                    FMRNRCRNGLGATKDGEPHYVVVHCTGYIKAWPPAGVSLPDDDPDAGQGSKFCLVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLCSSSLI----HNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LARENHSETERRRNKMTAYITELSDMVPTCSALARKPDKLTILRMAVSHM------
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                                                                                                                                                                                                                                                                                                                                                                    PVLNQPQSEWFGSTLYDQVHPDDVGKLREQLSTSENALTEGTKPWCLSNKDPAAPPES--
                                                                                                                                                                                                                                                                                                                                                                                                 PGTNF-SLELIGHSIFDFIHPCDQEELQDALTPRPN------LSKKKLEAPTERHF
                                                                                                                                                                                                                                                                                                                                                                                                                                    -KSLRGTGNTSTDGTYKPSFLTDQELKHLI----LEAADGFLFTVSCETGRVVYVSDSVT
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                                                                                                                                                                                                                                                                                                   ---ASKGRILDLKTGTVKKEGQQSMRMCMGSRRSFICRMRCGNSSVDAVSVNRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 142; DB 2; ilarity 20.5%; Pred. No. 0.00028; Conservative 43; Mismatches 95
                           Commun. 282, 487-492, 2001
ssion of negative ARNT2 factor disrupts
7633; MUID:21294759; PMID:11401485
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C;Accession: A56241
R;Reisz-Porszasz, S.; Probst, M.R.;
Mol. Cell. Biol. 14, 6075-6086, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aryl hydrocarbon receptor nuclear translocator protein - mouse C;Species: Mus musculus (house mouse)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
A56241
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C;Comment: This factor, a basic helix-loop-helix PAS (bHLH-PAS) factor, heterodimeriz
C;Genetics:
A;Gene: arnt2X
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-791 <REI>
A;Residues: 1-791 <REI>
A;Cross-references: GB:U10325; NID:g555687; PIDN:AAA56717.1; PID:g555688
A;Note: authors translated the codon TTT for residue 375 as Ser, TGT for
A;Note: authors failed to translate CAG for residue 507 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A56241;
A; Accession: A56241
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A; Residues: 1-392 <HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Identification of functional domains
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Best Local S
Matches 58
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Best Local Similarity
Matches 55; Conserv
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MCMGSRRSFICRMRCGTSSVDPVSMNRLSFLRNRCRNGLGSVKEGEPHFVVVHCTGYIKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF-SLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMRGTGNTSTDGAYKPSFLTEQELKHLI....LEAADGFLFVVAAETGRVIYVSDSVTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RENHSEIERRRNKMTQYITELSDMVPTCSALARKPDKLTILRMAVSHM------K
                                     ----ERHFSLRMKSTLTS-----
                                                                         PVLNQPQSEWFGSTLYDQVHPDDVDKLREQLSTSENALTGRVLDLKTGTVKKEGQQSSMR 254
                                                                                                               PGTNF-SLELIGHSIFDFIHPCDQEELQDALTPRPN-LSKKKLEAPT----
                                                                                                                                                     -KSLRGTGNTSTDGSYKPSFLTDQELKHLI----LEAADGFLFIVSCETGRVVYVSDSVT
                                                                                                                                                                                      GKRGRATGRILLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLCSSSLI----HNPT 129
                                                                                                                                                                                                                              LARENHSEIERRRRNKMTAYITELSDMVPTCSALARKPDKLTILRMAVSHM------ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EAPTERHFSLRMKSTLTSRGRT----LNLKAATWKVLHCSGHMRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNHPQSEWFGSTLFEQVHPDDVDKLREQLSTSENSMTGRILDLKTGTVKKEGQQSSMRMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-392 <HSU>
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                                                                                                                                                                                                                                                                                                        Conservative
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21.8%;
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                                                                                                                                                                                                                                                                                                        50; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 138.5; DB 2
Pred. No. 0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 138.5; DB 2
Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
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                                 -----RGRTLNLKAAT-----WKVLHCSGHMRA
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                                                                                                                     A;Gene: GDB:ARNT
A;Cross-references: GDB:119701; OMIM:126110
A;Map position: 1q21-1q21
                                                                                                                                                                                                                                                                                                                     C;Accession: I5950
R;Hoffman, E.C.; Reyes, H.; Chu, F.F.; Sander, F.; Conley, L.H.; Brooks, B.A.; Hankinson Science 252, 954-958, 1991
A;Title: Cloning of a factor required for activity of the Ah (dioxin) receptor. A;Reference number: I59550; MUID:91240280
A;Accession: I59550
                                                                                                                                                                                                                                                                                                                                                                                                                                                    aryl hydrocarbon receptor nuclear translocator Arnt [imported] - human c;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000 C;Accession: I59550
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A; Residues: 1-789 < RES>
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A; Residues: 1-776 <LIA>
A; Cross-references: GB:U14333
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                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches
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                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 HCTGYIKAWPPAGVSLPDDDPEAGQGSKFCLVAI 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 EGQQSSMRMCMGSRRSFICRMRCGTSSVDPVSMNRLSFLRNRCRNGLGSVKEGEPHFVVV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 ----HNPTPGTNF-SLELIGHSIFDFIHPCDQEELQDALTPRPN-LSKKKLEAPT----- 174
y Match 8.3%; Score 136.5; DB 2; Local Similarity 21.8%; Pred. No. 0.00084; hes 58; Conservative 50; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 HCSGHMRAYKPPAQTSPAGSPRS-EPPLQCLVLI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 -----KSLRGTGNTSTDGSYKPSFLTDQELKHLI----LEAADGFLFIVSCETGRV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 YKPPAQTSPAGSPRS-EPPLQCLVLI
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  Indels
                                            Length 789;
  57;
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  Gaps
  9;
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	315 WPPAGVSLPDDDPEAGQGSKFCLVAI 340	315	ŏ
	212 YKPPAQTSPAGSPRS-EPPLQCLVLI 236 ; ; ;	212	Ϋ́
314	DPVSVNRLSFVRNRCRNGLGSVKDGEP	255	ъ
211	175ERHESLRMKSTLTS	175	¥
254	195 PYLNOPQSEWFGSTLYDQVHPDDVDKLREQLSTSENALTGRILDLKTGTVKKEGQQSSMR 254	195	b
174	130 PGTNF-SLELIGHSIFDFIHPCDQEELQDALTPRPN-LSKKKLEAPT 174	130	¥
194	140 -KSLRGTGNTSTDGSYKPSFLTDQELKHLILEAADGFLFIVSCETGRVVYVSDSVT 194	140	b
129	74 GKRGRATGRILLPEGPGGFRHGTHRRGRHGLPYGKCQQAPGPQSVDLCSSSLIHNPT 129	74	¥
139	89 LARENHSEIERRRRNKMTAYITELSDMVPTCSALARKPDKLTILRMAVSHM 139	89	B
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Search completed: September 8, 2002, 07:39:34
Job time: 422 sec

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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1636
1 MALGLQRVRSNTELRKEKSR.....TESSLPSWVLWALNRKNCPG
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Copyright (c) 1993 - 2000 Compugen
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            ₽B
                            HIFA_HUMAN
PASI_MOUSE
PASI_HUMAN
NPAI_HUMAN
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SIM2_HUMAN
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SIM2_HUMAN
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TRH_DROME
CYCL_DROME
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ARNT_RAT
ARNT_HUMAN
TRH_DROME
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ARNT
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ALIGNMENTS

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Pfam; PF00785; PAC; 1.
Pfam; PF00999; PAS; 2.
PFINTS; PF01080; HYPOXIAIF1A.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
              DOMAIN
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    SEQUENCE
                                                                                                                   DNA_BIND
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                                                                                                                                                                                                                                    InterPro;
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PTM: REQUIRES PHOSPHORYLATION FOR DNA-BINDING.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH TRANSCRIPTION FACTORS.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: UBIQUITOUS.
DOMAIN: BOTH HYPOXIA RESPONSIVENESS AND TRANSACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Elemopean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIMERIZE WITH OTHER BHLH-PAS
                                                                                                                                                                                                                                                                                                                                                                                                                        AF004155; AAC53461.1;
AF004141; AAC53461.1;
AF004142; AAC53461.1;
AF004143; AAC53461.1;
AF004144; AAC53461.1;
                                                                                                                                                                                                                                                                                                                     AF004153;
AF004154;
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AF004146;
AF004147;
AF004148;
AF004149;
AF004150;
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Y09085; CAA70306.1;
Y13656; CAA70306.1; J0
Y09085; CAA70305.1; -
                                                                                                                                                                                                                                                                                              X95580; CAA64833.1; -. X95002; CAA64458.1; -.
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                                                                                                                                                                                                                                                                                                                                          AF004152;
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H PROTEIN. HETERODIMER OF AN ALPHA AND A BETA (ARNT) SUBUNITS. ALPHA SUBUNIT IS UNIQUE TO HIF-1 WHEREAS HIF-1 BETA (ARNT) CAN
                                                                                                                                       DNA-binding;
                                                                                                                                                                                                                                            IPR001321;
IPR001610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit
                     IPR000014;
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IPR001092; HLH_dim.
    822
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AAC53461.1;
AAC53461.1;
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AAC53461.1;
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AAC53461.1;
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    91858
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    ¥
HELIX-LOOP-HELIX MOTIF (BY SIMI PAS 1.
PAS 2.
PAC.
S -> T (IN REF. 1).
A -> T (IN REF. 2 AND 3).
I -> L (IN REF. 1).
E -> PALLOENVNTPNFSQ (IN REF. 2 K -> N (IN REF. 3 AND 4).
E -> V (IN REF. 4).
E -> V (IN REF. 4).
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ent is in
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MBL outstation -
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RESULT 2
HIFA_HUMAN
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Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIFA_HUMAN
Q16665;
Q1-NOV-1997
                                                                                     RUPERT J.L., Hochachka P.W.;
"HIFIA sequence in the Quechua, a high altitude population.";
"HIFIA sequence in the Quechua, a high altitude population.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES.
SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE ELEMENT (HRE).
-!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. HETERODINER OF AN ALPHA AND A BETA (ARNT) SUBUNITS.
THE ALPHA SUBUNIT IS UNIQUE TO HIF-1 WHEREAS HIF-1 BETA (ARNT) CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                         superfamily that interacts with components of the
                                                                                                                                                                                                                                                                                        MEDLINE-97236817; PubMed-9079689;
Hogenesch J.B., Chan W.K., Jackiw V.H.,
Pray-Grant M., Perdew G.H., Bradfield C.
"Characterization of a subset of the bas
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypoxia-inducible factor I alpha (HIF-I alpha) (ARNT interacting protein) (Member of PAS protein 1) (MOP1) (HIF1 alpha).
                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                             pathway.
                                                                                                                                                                                                                                                                                                                                                                                                 Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;
"Hypoxia inducible factor 1 is a basic-helix-loop-helix-PAS
heterodimer regulated by cellular 02 tension.";
Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95296340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIF1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
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                         DIMERIZE WITH OTHER BHLH-PAS PROTEINS. INTERACTS SUBCELLULAR LOCATION: Nuclear (Potential). TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. HI KIDNEY AND HEART.
INDUCTION:
DOMAIN: BOT
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               UNDER REDUCED
                                                                                                                                                                                                                                              272:8581-8593(1997).
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HYPOXIA RESPONSIVENESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7539918;
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Pred. No. 2.3e-35;
Pred. No. 2.3e-35;
              OXYGEN TENSION
                                                                                                                                                                                                                                                                                            of the basic-helix-loop-helix-PAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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AND
                                                                                                                                                                                                                                                                                                        Brown R.C.,
.A.;
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TRANSACTIVATION CAPABILITY
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RESULT 3
PAS1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
InterPro; IPR001321; Hypoxind.
InterPro; IPR001610; PAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European
                                                                                                                                                                                                                                                                                                                                                        NTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                   LICEPIP 228
                                                                                                                                                                                                     DGDMIYISDNVNKYMGLTQF
                                                                                                                                                                                                                   SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT
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                                                                                                  LICEAIP
                                                                                                                                                    ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV 234
                                                                                                                                                                                                                                                                                                   AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA--
                                                                                                                                                                                                                                                                                                                                      SSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLL 73
                                                                                                                                  QRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCG--YKKPPMTCLV
                                                                                                                                                                                                                                                                                                                                                                                                         114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U29165; AAC51210.1; -. AF207601; AAF20139.1; -. AF207602; AAF20140.1; -. AF208487; AAF20149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00086; PAC;
SM00091; PAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE WITHIN THE C-TERMINAL PART.
REQUIRES PHOSPHORYLATION FOR DNA-BINDING.
LARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Phosphorylation.

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826 AA; 92670 M
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92670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HypoxindFlA. PAC.
                                                                                                                                                                                                                                                                                                                                                                                                                        30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
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                                                                                                                                                                                                  -ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNT
                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC DOMAIN.
HELIX-LOOP-HELIX PAS 1.
PAS 2.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 495; DB 1;
Pred. No. 2.3e-35;
5; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABD4F7DAA135BE2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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Mech. Dev. 63:51-60(1997).

-I- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES. SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE ELEMENT (HRE), REGULATES THE VASCULAR ENDOTHEIAL GROWTH FACTOR (VEGF) EXPRESSION AND SEEMS TO BE IMPLICATED IN THE DEVELOPMENT OF BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE BLOOD VESSELS AND THE BLOOD PLAY A ROLE BLOOD PLAY 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAS1_MOUSE STANDARD; PRT; 874 AA.
P97481; 008787; 055046;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Endothelial PAS domain protein 1 (EPAS-1) (HIF-1 alpha-like factor)
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Risan ש ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain capillary; MEDLINE=97321546; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97152468; PubMed=9000051;
Tian H., McKnight S.L., Russell D.W.;
"Endothelial PAS domain protein 1 (EPAS1), a
selectively expressed in endothelial cells.";
Genes Dev. 11:72-82(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "HRF, a putative basic helix-loop-helix-PAS-domain transcription factor is closely related to hypoxia-inducible factor-1 alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ema M., Taya S., Yokotani N., Fujii-Kuriyama Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97272213;
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MEDLINE=97152468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MHLF) (HIF-related factor) (HRF).
                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. HIGHEST TO HIF-1 ALPHA.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad.
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niormatics Institute. There are no restrictions it institutions as long as its content is in statement is not removed. Usage by
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        is not removed. Usage by and for commercia agreement (See http://www.isb-sib.ch/announce,
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Matches 115;
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InterPro; IPR003015; HLH_M
InterPro; IPR00301092; HLH_d
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00785; PAC; 1.
SMART; SM00353; HLH; 1.
SMART; SM00365; PAS; 2.
SMART; SM00091; PAS; 2.
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MGD; MGI:109169;
Q99814; Q99630;
          PAS1_HUMAN
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Activator; Angiogenesis; Devel
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                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                       IIMCEPI-QHPSH
                                                                                                    ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKP-PAQTSPAGSPRSEPPLQCL
                                                                                          ERDFFMRMKCTVTNRGRTVNLKSATWKVLHCTGQVRVYNNCPPHSSLCGS--KEPLLSCL
                                                                                                                              GDMIFLSENISKFMGLT-QVELTGHSIFDFTHPCDHEEIRENLTLKNGSGFGKKSKDVST
                                                                                                                                                                ISFLRTHKLLSSYCSENESEAEADQQM------DNLYLKALEGF
                                                                                                                                                                           ISYLRMHRL----CAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQS
                                                                                                                                                                                                    MTADKEKKRSSSELRKEKSRDAARCRRSKETEVFYELAHELPLPHSVSSHLDKASIMRLA
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D89787;
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                                                                                                                                                                                                                                                                                             Conservative
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BAA20130.1; -
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           STANDARD;
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45.5%;
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33;
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C -> S (IN REF. 2).

K -> KS (IN REF. 3).

K -> KS (IN REF. 3).

VS -> AA (IN REF. 3).

G -> V (IN REF. 2).

A -> P (IN REF. 2).

A -> L (IN REF. 1).

P -> L (IN REF. 1).

P -> L (IN REF. 3).

A -> G (IN REF. 3).

D -> E (IN REF. 3).

D -> L (IN REF. 3).
                                                                                                                                                                                                                                                 Score 488; DB 1
Pred. No. 1e-34;
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PAS 1.
PAS 2.
PAC.
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           PRT;
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R SMART; SM00086; PAC; 1.

JR SMART; SM00091; PAS; 2.

DR PROSITE; PS000038; HELIX_LOOP_HELIX; 1.

DR PROSITE; PS50112; PAS; 2.

DR PROSITE; DNA-binding; Nuclear protein; Transcription received the protein of the pro
                                    Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
SMART; SM000353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97152468; PubMed-9000051;
MEDLINE-97152468; PubMed-9000051;
Tian H., McKnight S.L., Russell D.W.;
"Endothelial PAS domain protein 1 (EPAS1), a transcription factor
"Endothelial PAS domain protein 1 (EPAS1), a transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998
15-DEC-1998
01-MAR-2002
Endothelial
                                                                                                                                                                                                                                                                                                           Interpro; IPR003015; IInterpro; IPR001092; IInterpro; IPR001610; IInterpro; IPR00014; Interpro; IPR000014; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
Pray-Grant M., Perdew G.H., Bradfield C.A.;
"Characterization of a subset of the basic helix-loop-helix-PAS
superfamily that interacts with components of the dioxin signaling
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U81984; AAB41495.1; EMBL; U51626; AAC51212.1;
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SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES, WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMIL TRANSCRIPTION FACTORS. HIGHEST TO HIF-1 ALPHA. SIMILARITY: CONTAINS 2 PAS (PER ARMY-SIM) DIMERIZATION DOMAINS SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. HETERODIMER WITH THE ARNT PROTEIN.
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(Rel. 37, La
(Rel. 41, La
(PAS domain)
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Chordata;
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HLH_dim.
PAC.
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Last annotation update)
n protein 1 (EPAS-1) (Member of PAS protein
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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DOMAIN
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                                                                                                                                              MEDLINE-97165088; PubMed-9012850;
Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Fran
Shelton J., Richardson J., Russell D.W., McKnight S.L.,
"Molecular characterization of two mammalian bHLH-PAS of
selectively expressed in the central nervous system.";
Proc. Natl. Acad. Sci. U.S.A. 94:713-718(1997).
 "Characterization of a subset of the basic-helix-loop-helix-PAS superfamily that interacts with components of the dioxin signal
                                     TISSUE-Hepatoma;
MEDLINE-97236817; PubMed-9079689;
Hogenesch J.B., Chan W.K., Jackiw V.H.,
Pray-Grant M., Perdew G.H., Bradfield C.
                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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Pred. No. 6.7e-33;
4; Mismatches 82
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Catarrhini; Hominidae
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                                       Brown R.C.,
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InterPro; IPR001092; HLH_d
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAS.
InterPro; IPR000014; PAS.
Pfam; PF00989; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_LO
PROSITE; PS00038; HELIX_LO
PROSITE; PS00112; PAS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Potential). SIMILARITY: BELONGS TO THE BASIC HELIX-LOCTRANSCRIPTION PACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: EFFICIENT BHLH PROTEIN.
CES
                                                                                                                                    RKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGG
                     CEA
                                                                                                                                                                                                        KRG--RATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGP---QSVDLCSSSLIHNPT 129
                                                                                                                                                                                                                               RKEKSRNAARSRRGKENLEFFELAKLLPLPGAISIQLDKASIVRLSVTYLRLRRFAALGA 105
                                            SGYKVIHVTGRLRAHALGLVALGHTLPPA-----PLAELPLHGHMIVFRLSLGLTILA
                                                                  ATWKVLHCSGHMRAYK----
                                                                                        PPTPSSVSSSSSSSSSLADTPEIEASLTKVPPSSLVQERSFFVRMKSTLTKRG--
                                                                                                                                                                                   PPWGLRAAG-----PPAGLAPG--RRGPAALVSEVFEQHLGGHILQSLD----
                                                                                                                                                                                                                                                                             l Similarity
97; Conserv
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211
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AAC51214.1; -.
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HLH_dim.
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GARPAGGPGSOPP (IN REF. 2).
T -> P (IN REF. 2).
S -> P (IN REF. 2).
V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                   r protein; Transcription I
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (
PAS 1.
PAS 2.
PAC.
                                                                                                                                                                                                                                                                                        Score 294; DB 1;
Pred. No. 4.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER
                                                                                                                                                                                                                                                                                                                                  S -> P (IN REF. 2).
S -> P (IN REF. 2).
V -> A (IN REF. 2).
E1EFB50040A2E7D1
                                                                                                    -----TERHFSLRMKSTLTSRGRTLNLKA
                                                                   PPAQTSPAGSPRSEPPLQ
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                                                                                                                                                                                    a collaboration - MBL outstation -
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Best Local
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or send a
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the Euro
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                                                                                                                                                                                                                                                                                InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPA1_MOUSE
                                                                                                                                                                                                                                            SMART; SM000353; HLH;
SMART; SM00086; PAC;
SMART; SM00091; PAS;
                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97165088; PubMed=9012850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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16-OCT-2001
                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                    PROSITE; PS00038; HELIX_LOOP_HELIX; PROSITE; PS50112; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:109205; Npas1
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                                                                                                                                                                                                         Repeat;
46
                         15
                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear TISSUE SPECIFICITY: IN BRAIN, SPINAL CORD.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAY
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RKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGG 74
                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                        DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
s domain protein 1 (Neuronal PAS1)
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                             AAB47247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FACTORS.
                                                                                                               58 B. 99 H. 2005 P. 360 P. 409 P. 223 P. 63736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                             17.9%;
33.1%;
                                                                                                                                                                                                         Nuclear
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                                                                                                                                        r protein; Transcrit
BASIC DOMAIN.
HELIX-LOOP-HELIX N
PAS 1.
PAS 2.
PAC.
                                                             Score
Pred.
                                                                                                                POLY-SER.
D6477696DF69A4B3 CRC64;
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                                                   Mismatches
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EXCLUSIVELY NEURONAL. ALSO FOUND
                                                             293.5; DB 1;
No. 5.1e-18;
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                                                                                                                                                                                 SIMILARITY)
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        RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D.) (Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Adams M.D.) (Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Adams M.D.) (Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P., Rottier P., Rottier P., Rottier R., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup I..E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Borshin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Glasser K., RA Harris M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A., RA Mount S.M., Mothra C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMA_DROME STANDARU
Q24167; Q9VAA5;
15-DEC-1998 (Rel. 37, C
16-OCT-2001 (Rel. 40, I
16-OCT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nambu J.R., Chen W., Hu S., Crews S.T.;
"The Drosophila melanogaster similar bHLH-PAS gene encodes a protein related to human hypoxia-inducible factor 1 alpha and Drosophila single-minded.";
Gene 172:249-254(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similar protein.
SIMA OR CG7951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-96269413; PubMed-8682312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Drosophilidae; Drosophila.
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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yell J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:1185-2195(2000).
CC --- SUBUNIT: EFFICIENT DNA BINDING TRANSCRIPTIONAL ACTIVATOR.
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Pfam; PF00989; PAS; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Unpublished results,
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Wang Y., Shimizu N.,
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15-JUL-1999 (Rel. 38,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                     Jenkins N.A., Crews
Tessier-Lavigne M.;
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Fan C.-M., Kuwana
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Jenkins N.A., Crews S., Martinez S.,
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RELAQKVKDEPQQNSGVSTHHRDLFVRLKCTLTSRGRSINIKSASYKVIHITGHL
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                                                                                                                                                                                                                                                                                                                                 RRNNEKRKEKSRDAARCRRSKETEIFMELSAALPLKTDDVNQLDKASVMRITIAFLKIRE
                                                                                                                                                                                                                                                                                                                                                             RSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMFLTISYLRMHR
                                                                                                               LKQTMDGFLLVLSHEGDITYVSENVVEYLGITKIDTLGQQIWEYSHQCDHAEIKEALSLK
                                                                                                                                                                                                                       MLQFVPSLRDCNDDIKQDIETAE------DQQEVKPKLEVGTEDWLNGAEAREL
                                                                                                                                                                                                                                                                          -CAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDL
                            -RHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHM
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Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Copeland N. Rubenstein
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                                                                                                                                                      SMART; SM00353; HLH;
SMART; SM00086; PAC;
SMART; SM00091; PAS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION FACTORS.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHE BILL PROTEIN. HETERODIMER OF SIM AND ARMY.

1- TISSUE SPECIFICITY: DEFRECTED IN LUNG, SKELETAL MUSCLE AND KIDNEY DURING FETAL DEVELOPMENT IT IS FOUND IN THE CNS, DEVELOPING KIDNEY, MESODERMAL AND ENDODEMAL TISSUES, INCLUDING DEVELOPING SOMITES, MESONEPHRIC DUCT, AND FOREGUT.

1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
                                                  Transcription
                                                                                 Developmental
                                                                                                                                                                                                                                PRINTS; PR00785; NCTRNSLOCATR.
                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=129/SV;
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Saijoh Y., Fujii H.,
"Two new members of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 7:615-624(1997)
                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97172525;
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L; D79209; BAA11467.1; -. AB013491; BAA28270.1; -. AB013494; BAA28270.1; JOINED.
L; AB013485; BAA28270.1; JOINED.
L; AB013485; BAA28270.1; JOINED.
L; AB013487; BAA28270.1; JOINED.
L; AB013488; BAA28270.1; JOINED.
L; AB013489; BAA28270.1; JOINED.
L; AB013489; BAA28270.1; JOINED.
L; AB013489; BAA28270.1; JOINED.
L; AB013489; BAA28270.1; JOINED.
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FUNCTION: TRANSCRIPTIONAL FACTOR THAT MAY HAVE PLEIOTROPIC DURING EMBRYOGENESIS AND IN THE ADULT.
                                                                                                                                                                                                                                   ; PF00989; PAC;
; PF00989; PAS; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; AB013489; BAA28270
; AB013490; BAA28270
MGI:98306; Sim1.
                                                                                                    PS00038; HELIX_LOOP_HELIX; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                  IPR003015; HLH_Myc.
IPR001092; HLH_dim.
IPR001067; Nuctrnslocator.
                                                                                                                                                                                                                                                                                                        IPR001610; PAC. IPR000014; PAS.
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                                               regulation; DNA-binding
                                                                          protein; Neurogenesis; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     show different expression patterns during
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, Hamada H., Kikuchi Y., Fujii-Kuriyama Y.;
the murine Sim gene family are transcriptional
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                       MEDLINE-97343329; PubMed-9199934;
Chrast R., Scott H.S., Chen H., Kudoh J., Rossier C.,
Chrast R., Scott H.S., Chen H., Kudoh J., Rossier C.,
Minoshima S., Wang Y., Shimizu N., Antonarakis S.E.;
"Cloning of two human homologs of the Drosophila single-minded
SIM1 on chromosome 6q and SIM2 on 21q within the Down syndrome
SIM1 on chromosome 6q and SIM2 on 21q within the Down syndrome
chromosomal region.";
Genome Res. 7:615-624(1997).

-I- FUNCTION: TRANSCRIPTIONAL FACTOR THAT MAY HAVE PLEIOTROPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
single-minded homolog 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jing.
SIM1.
Homo sapiens (Human).
Homo sapie
                 EMBL; U70212; AAB62395.1; MIM; 603128; -.
                                                                                         entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
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                                                                                            an email to license@isb-sib.ch).
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PAS 2.
H -> L (IN REF. 1).
H -> PAS (IN REF. 1).
P -> R (IN REF. 1).
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Pred. No. 1
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                                                                                                                     (See http://www.isb-sib.ch/announce/
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RESULT 10
SIM2_MOUSE
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Best Local S
Matches 76
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InterPro; IPR001610; PAC.
InterPro; IPR00014; PAS.
Pfam; PF00785; PAC; 1.
Pfam; PF00789; PAS; 2.
SMART; SM00093; HLH; 1.
SMART; SM00096; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q61079; Q61904; Q61046;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last seg
16-OCT-2001 (Rel. 40, Last ann
Single-minded homolog 2 (SIM t
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DOMAIN
SEQUENCE
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DNA_BIND 1 13 BASIC DOMAIN.
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SEQUENCE FROM N.A.
STRAIN-SWISS WEBSTER;
                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIM2_MOUSE
                                                                                                                                                                                                                                                                                                                       MOffett P., Dayo M., Reece M., McCormack M.K., "Characterization of msim, a murine homologue of the control of 
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fetal kidney;
MEDLINE=96299751; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                              MEDLINE=96144720;
                                                                                                                                                                                                                                                                                               transcription factor.
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                                                              M., Suzuki M., Morita M., Hirose K., Sogawa K., Matsuda Y., h O., Saijoh Y., Fujii H., Hamada H., Fujii-Kuriyama Y.; A cloning of a murine homologue of Drosophila single-minded, its expression in mouse development, and chromosome localization."; hem. Biophys. Res. Commun. 218:588-594(1996).
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                                                                                                                                                                                     PubMed=8561800;
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                                                                                                                                                                                                                                                                                                                                                               PubMed=8661115;
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Rodentia;
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Last annotation update)
2 (SIM transcription factor) (mSIM).
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                                                                                                                                                                                                                                                                                                                       , Pelletier J.;
of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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InterPro; IPR001610; PAC
InterPro; IPR000014; PAS
Pfam; PF00785; PAC; 1.
Pfam; PF00785; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
DOMAIN
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CONFLICT
                                                                                                                                                                                                      InterPro;
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EMBL;
EMBL;
MGD; N
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. BIOL. Chem. 273:4451-4457(1997).

J. BIOL. Chem. 273:4451-4457(1997).

FUNCTION: TRANSCRIPTION FACTOR THAT MAY HAVE PLEIOTROPIC DEVELOPMENT IN COOPERATION WITH ARNT. IT MAY HAVE PLEIOTROPIC EFFECTS IN THE TISSUES EXPRESSED DURING DEVELOPMENT.

FOR SUBURIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH AND BHLH PROTEIN. HETERODIMER OF SIM2 AND ARNT.

FISSUE SPECIFICITY: TRANSCRIPTS WERE DEFCTED IN HIGH LEVELS KIDNEY FOLLOWED BY SKELETAL MUSCLE AND LUNG. LOW LEVELS WERE IN TESTIS, BRAIN AND HEART: IN EARLY FETAL DEVELOPMENT IT IS IN CNS, DEVELOPING KIDNEY, TONGUE EPITHELIUM AND CARTILAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diencephalic expression indicate a syndrome.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ICR X SWISS WEBSTER; TISSUE-Embryo; MEDLINE-96299750; PubMed-8661114; Yamaki A., Noda S., Kudoh J., Shindoh N., Kawasaki K., Shimizu Y., Shimizu N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single-minded suggest possible roles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97020303; PubMed-8812055;
Fan C.M., Kuwana E., Bulfone A.,
Jenkins N.A., Crews S., Martinez
Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97172525; PubMed=9020169;
Probst M.R., Fan C.M., Tessier-Lavigne M., Hankinson
"Two murine homologs of the Drosophila single-minded
interact with the mouse aryl hydrocarbon receptor nu
                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                  Transcription
                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translocator protein."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 35:136-143(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression patterns of two
                                                                                             Developmental
                                                                                                                                                                                                                                                         BL; U42554; AAB19098.1; -.
BL; D63383; BAA09700.1; -.
BL; U40576; AAA91202.1; -.
BL; D64135; BAA11013.1; -.
D; MGI:98307; Sim2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSCRIPTION FACTORS.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogenesis
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SIMILARITY: BELONGS TO THE BASIC
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PS50112; PAS; 2.
Hental protein; Neurogenesis; Nuclear
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263 336
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HLH_dim.
PAC.
PAS.
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                                                                                  DNA-binding
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PAS 1
PAS 2
K ->
                                                      BASIC DOMAIN.
HELIX-LOOP-HELIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fletcher C.F., S., Puelles L.
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, Rubenstein
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Eukaryota; Futheria; Primates;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Single-minded homolog 2.
  Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20289799;
                                                                                                                                                                                            Shibuya K., Kudoh J., Minoshima S., Kawasaki F
Shintani A., Asakawa S., Shimizu N.;
"Genomic sequencing of 1.2-Mb region on human
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                 CLIONING of two human homologs
SIM1 on chromosome 6q and SIM2
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MEDLINE=97343329; PubMed=9199934;
Chrast R., Scott H.S., Chen H., Kudoh J.,
Wang Y., Shimizu N., Antonarakis S.E.;
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S -> T (IN REF. 3).
P -> R (IN REF. 3).
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A -> R (IN REF. 2).

APPHYLGASVIITNGR -> PPTALLDGRLGHHHOROVTRO SRSAGRPSGRSHROAFSGSSFTPKVOOMEGRTVYARYKLIY TETTILLELRSKLLDFYRCWCRGLGRSWEMGRGTAHSCPR AGFHÖALHGVIL (IN REF. 3).

C7904CD24COABBAF CRC64;
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D44448; BAA07909.1; -.

D44448; BAA07910.1; -.

D44448; BAA07910.1; -.

D70838; BAA11108.1; -.

AP000697; BAA89433.1; -.

AP000697; BAA89433.1; -.

NOT_ANNOTATED_CDS

AB003185; BAA21489.1; -. AB003185; BAA21490.1; -. U80456; AAB62396.1; U80457; AAB62397.1;

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Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Shintani A., Sasaki T., Nagamine K., Mitsuyama S. Minoshima S., Shimizu N., Nordsiek G., Hornische Scharfe M., Schoen O., Desario A., Reichelt J., Ramser J., Beck A., Klages S., Hennig S., Riesse Wehrmeyer S., Borzym K., Gardiner K., Nizetic D. Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
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an email to
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., Shimizu Y., Shimizu N.;
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SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                 TRH_DROME STANDARD; PRT; YOU AM (224119; Q24165; Q59007; O1-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein;
Transcription regulation
                                                                                                                                    Trachealess protein.
Trachealess protein.
TRH OR CG6883.
TRH OR CG6883.
Diosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00038; HELIX PROSITE; PS50112; PAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
Wilk R., Weizman I., Shilo B.-Z.
"Trachealess encodes a bHLH-PAS
tracheal cell fates in Drosophil
Genes Dev. 10:93-102(1996).
                                                     TISSUE=Embryo;
MEDLINE=96136712; PubMed=8557198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                    166
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                                                                                                                                                                                                                                                                                                                                   CVLAK -- RNAGLTCSGYKVIHCSGYLK 190
                                                                                                                                                                                                                                                                                                                                                             STLTSRGRTLNLKAATWKVLHCSGHMR
                                                                                                                                                                                                                                                                                                                                                                                                        LGDAWGQ -- PSRAGPLDGVAKELGSHLLQTLDGFVFVVASDGKIMYISETASVHLGLS --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEKSKNAAKTRREKENGEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRAVFPEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGRATGRLLPEGPGGFRHGTHRRGRHGLPV-----GKCQQAPGPQSVDLCSSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGGK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
73; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001092; HLH_dim.
IPR001610; PAC.
IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003015; HLH_Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation; DNA-bi
                                                                                                                                                                                                                                                                                                                                                                                        -QVELTGNSIYEYIHPSDHDEMTAVLTAHQPLHHHLLQEYEIERSFFLRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HELIX_LOOP_HELIX;
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73218
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54
149
288
667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%;
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            Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQTCPLSASK (IN ISOFORM SIM2S). IH -> RI (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAASGLACAPGGPEAATGALRLRHPSPAATSPPGAPLPHYL
GASVIITNGR -> HFFSSKKPMLPAKFGQPQGSPCEVARF
FLSTMPASGECQWHYANPLVPSSSSPAKNPPEPPANTARHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEDTAPPSFPSCGHYREEPALGPAKAARQAARDGARLALAR
AAPECCAPPTPEAPGAPAQLPFVLLNYHRVLARRGPLGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAS 1.
PAS 2.
VFSSKKPMLPAKFGQPQGSPCEVARFFLSTLPASGECOWHY
ANPLVPSSSSPAKNPPEPPANTARHSLVPSYEAPAAAVRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVPSYEGGSGLLVGKVGGLRTAGSRSSHGGGWQMETEPSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC
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                 protein la.";
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No. 1.
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                           that
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.1e-14;
                           S
                                                                                                                                      Brachycera; Muscomorpha;
                           an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 667;
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                           inducer
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                                                                                                                                                                                                                                                                                                                                                                                                                  183
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RA Brandon R.C., Kogers Y.H.C., Blazel R.G., Champe M., Pfeliffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Kelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Kelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Kelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baldwin D., Ballwin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Houst D., L., Hernandez J.R., Houck J., Ra Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Ra Hostin D., Holty D., Kraft C., Kraft S., Kilp D., Lai Z., Ra Hostin D., Holty D., Kraft C., Kraft S., Kilp D., Lai Z., Ra Hostin D., Holty D., Kraft C., Kraft S., Kilp D., Lai Z., Ra Hostin D., Lei Y., Lavitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Hortin D., Holty D., Kraft C., Kraft S., Kilp D., Lai Z., Ra Kimmel B.E., Kodira C.D., Kraft C., Kraft S., Kilp D., Lai Z., Ra Hostin D., Lei Y., Lavitsky A.A., Li J., Li Z., Liang Y., Hallwin S., W., Walson K., Hubary C., Hottin S., Kilp D., Lai Z., Liang Y., Lin X., Ra Hortin D., Karpen G.H., Karpen G.H., Karpen G.H., Ra Hortin D., Karpen G.H., Karpen J., Pari Y., Ress M.G., Ra Hortin D., Karpen G., Stapleton M., Skupski M.P., Smith T., Ra Palazzolo M., Palazzolo M., Shipski M.P., Smith T., Ra Palazzolo M., Palazzol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       George R.A., Lewis S.E., Richards S., Ashburner M., Hend
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Tubulogenesis in Drosophila: a requirement for the trachealess gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isaac D.D., Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96136713; PubMed=8557189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BY STAGE 12, EXPRESSION IS CONFINED TO SIMILARITY: BELONGS TO THE BASIC HELLY TRANSCRIPTION FACTORS.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-S SIMILARITY: CONTAINS 1 PAS-ASSOCIATED CAUTION: REF-2 SEQUENCE DIFFERS FROM IN POSITIONS 22 TO 34.
                                                                                                 DEVELOPMENTAL STAGE: DURING EMBRYOGENESIS, FIRST DETECTED IN THE TRACHEAL PLACODES AT STAGE 8, AND EXPRESSION CONTINUES THROUGHOUT EMBRYONIC AND LARVAL DEVELOPMENT. IN THE DEVELOPING SALIVARY GLAND, EXPRESSION IS OBSERVED IN THE ENTIRE GLAND AT STAGE 9 AND BY STAGE 12, EXPRESSION IS CONFINED TO THE SALIVARY DUCTS.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10:103-117(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOLt
                                                         (PER-ARNT-SIM) DIMERIZATION DOMAINS.
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Hoskins R.A.,
                       THAT
                                        C-TERMINAL (PAC)
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Best Local
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Pfam; PF00989; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_PROSITE; PS00112; PAS; 2.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                        313
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                AGSPRSEPPLQCLVLICEAIPQLPFHD
                                                                                            TLTSRGRTLNLKAATWKVL
                                                                                                                                                                                                              VSIYLGLS----
                                                                                                                                                                                                                                                  QSVDLCSSSLIHNPTPGTNFSLELIGHSIFDFIHPCDQEELQDAL---
                                                                                                                                                                                                                                                                                    GDPPWTREASSSSKLKSAAIRRSPAVDLFEQHQGTHILQSLDGFALAVAADGRFLYISET 204
                                                                                                                                                                                                                                                                                                                                                                                                      ELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMH-----
                                                        TLTKRG--CHFKSSGYRASDATSNCNNGNNASNNAKNVKNPGSNYSVVLLLCKLRPQYTF
                                                                                                                                  SSGGGGGGAGGGMASPTSGASDDGSGTHGTNNPDVAASMTQASTSGYKGYDRSFCVRMKS
                                                                                                                                                                                                                                                                                                                                                                ELRKEKSRDAARSRRGKENYEFYELAKMLPLPAAITSQLDKASIIRLTISYLKLRDFSGH 144
                                                                                                                                                                                                                                                                                                                          -----RLCAAGGKRGRATGRLLPEGPGGFRH-GTH-RRGRHGLPV-----GKCQQAPGP 114
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U42699; AAA96754.1; ALT_FRAME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001610; PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001092; HLH_dim.
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nilarity 27.2%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102241
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=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 251; DB 1;
; Pred. No. 4.5e-14;
41; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY.

POLY-GLY.

MISSING (IN ISOFORM 3).

MISSING (IN REF. 1).

P -> A (IN REF. 2).

G -> GG (IN REF. 1).

A -> P (IN REF. 1).

A -> V (IN REF. 1).

MW; 8F9CF758F1370541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tive splicing.
BASIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
POLY-GER.
POLY-GLY.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAS
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                                                                                                                                                                      --TPRPNLSKKKLEAPT----
                    247
                                                                                            HCSGHMRAYKPPA----
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01-NOV-1988 (Rel. 09, 0

01-MAY-1992 (Rel. 22, 1

16-OCT-2001 (Rel. 40, 1
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                                        Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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"Specification of the Drosophila CNS midline cell lineage: direct control of single-minded transcription by dorsal/ventral patterning."
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Nambu J.R., Lewis J.O., Wharton
"The Drosophila single-minded ge
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MEDLINE=92103681; PubMed=1760843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity
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InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00989; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00086; PAS; 2.
PROSITE: PS000097
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PROSITE; PS00038; HELIX_LOOP_HELIX; 1.

PROSITE; PS50112; PAS; 2.

Developmental protein; Neurogenesis; Nuclear protein; Repeat;
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InterPro; IPR003015; HLH_1
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                                  KEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGGK 75
KEKSKNAARTRREKENTEFCELAKLLPLPAAITSQLDKASVIRLTTSYLKMRQVFPDG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation;
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148
312
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                                                                                                                                                                                                                                                                      73589
                                                                                                                                              15.2%;
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POLY-ASN.
POLY-GIN.
POLY-GIN.
POLY-SER.
POLY-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALT_SEQ.
ALT_SEQ.
                                                                                                            Score 249; DB 1; 1
Pred. No. 4.4e-14;
9; Mismatches 84;
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POLY-VAL.
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                                                                                                                                                                      Length 673;
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CYCL_DROME
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C. Baldwin D.,
B Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
B Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
B Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
B Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Chandra J., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Da Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain, and Muscle;
MEDLINE-98279147; PubMed-9616122;
Darlington T.K., Wager-Smith K., Ceriani M.F., Staknis D., Gekakis
Steeves T.D.L., Weitz C.J., Takahashi J.S., Kay S.A.;
Steeves T.D.L., Weitz C.J., Takahashi J.S., Kay S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYCL_DROME STANDARD; PRT; 413 AA. 061734; 076344; 0997444; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98252178; PubMed-9630224; Rutila J.E., Suri V., Le M., So W.V., Rosbash M., Hall J.C.; "CYCLE is a second bHLH-PAS clock protein essential for circadian rhythmicity and transcription of Drosophila period and timeless." Cell 93:805-814(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cycle protein (Brain and muscle ARNT-like 1) (BMAL1) (MOP3). CYC OR CG8727.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Closing the circadian loop: CLOCK-induced transcription of its own inhibitors per and tim.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGRATGRLLPEGPGGFRHGTHRR-GRHGL------PVGKCQQAPGPQSVDLCSSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ors per and tim.";
280:1599-1603(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JUN-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases.
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RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Tunner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -i- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR INVOLVED IN THE GENERATION
OF BIOLOGICAL RHYTHMS. ACTIVATES CYCLING TRANSCRIPTION OF PERIOD
CC (PER) AND TIMELESS (TIM) BY BINDING TO THE E-BOX (3'-CACGTG-5')
PRESENT IN THEIR PROMOTERS. CYC MUTANTS DON'T DISPLAY PER AND TIM
CC CYCLING, AND ARE COMPLETELX ARRHYTHMIC.
CC -I- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. FORMS A HETERODIMER WITH CLOCK IN ORDER TO ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris N.L.,
Hostin D., Ho
Jalali M., Ka
Kimmel B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or-send an email to license@isb-sib.ch).
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                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0023094; cyc.
InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
InterPro; IPR001067; Nuctrnslocator.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
CONFLICT
                                                                                                                                                                                                                                                                                                                          SMART; SM00353; HLH;
SMART; SM00086; PAC;
SMART; SM00091; PAS;
                              CONFLICT
                                                          DOMAIN
                                                                                                                                                                                                                      Biological
                                                                                                                                                                                                                                            Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00785; NCTRNSLOCATR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear (Potential).

TISSUE SPECIFICITY: EXPRESSED AT LEAST IN HEAD AND OVARY.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY

TRANSCRIPTION FACTORS. HOMOLOG OF HUMAN BMALL PROTEIN.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00010; HLH; 1.
PF00989; PAS; 2.
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P22415; 12
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PS50112; PAS;
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242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; AAC39124.1; -.; AAC62235.1; -.; AAD10629.1; -.; AAF49107.1; -.
     43
175
367
413
234
242
                                                                                                                                                                                                                                                                                              _LOOP_HELIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                            DNA-binding; Repeat;
  POLY-SER.
S -> T (I
H -> Y (I
                                                                                                       HELIX-LOOP-HELIX MOTIF.
PAS 1.
PAS 2.
  Y (IN
     REF.
                                                                                                                                                                                                                                            Nuclear protein;
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RESULT 15
ARNT_MOUSE STANDARD;
ID ARNT_MOUSE STANDARD;
AC P53762; Q60661;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-VV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aryl hydrocarbon receptor nuclear translocator (ARNT protein) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1 beta)

**eceptor.oran).**

**Peceptor.oran).**

**Vertebrata; Euteleostomi;
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SEQUENCE
                                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                                                                                                                                         Reisz-Porszasz S., Probst M.R., Fukunaga B.N., Hankinson "Identification of functional domains of the aryl hydrocz receptor nuclear translocator protein (ARNT)."; Mol. Cell. Biol. 14:6075-6086(1994).
                                                                                                                                                                                                                                           Li H., Dong L., Whitlock J.P. Jr.; "Transcriptional activation function
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (LONG
                                                                                                                                                                                                                          translocator.";
                                                                                                                                                                                                                                                                             MEDLINE=95050586;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94344118; PubMed=8065341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
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SUBCELULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUS.
                                                          OF PAH PROCARCINOGENS.
SUBBURIT: EFFICIENT DAA BINDING REQUIRES
BHLH PROTEIN. FORMS AN HETERODIMER WITH
WITH OTHER BHLH PROTEINS. INTERACTS WITH
COLLED-COLL CONTAINING PROTEIN 3.
                                                                                                                                      BIOL. Chem. 269:28098-28105(1994).

BIOL. Chem. 269:28098-28105(1994).

FUNCTION: REQUIRED FOR ACTIVITY OF THE AH (DIOXIN) RECEPTOR. THIS PROTEIN IS REQUIRED FOR THE LIGAND-BINDING SUBUNIT TO TRANSLOCATE FROM THE CYTOSOL TO THE NUCLEUS AFTER LIGAND BINDING. THE COMPLEX THEN INITIATES TRANSCRIPTION OF A GENES INVOLVED IN THE ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTSDENRKQNHSEIEKRRRDKMNTYINELSSMIPMCFAMQRKLDKLTVLRMAVQHLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-TWKYLHCSGHMRAYKP-PAQTSPAGSPRSEPPLQCLYLICEAIPQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDSVSSVLNST-----QADLLGQSWFDVLHPKDIGKVKEQLSSLEQCPRERLIDAKTMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- SSSLIHNPTPGTNFSLELIGHSIFDFIHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YKTDVPQSLCRLCPGARRSFFCRMKLRTASNNQIKEESDTSSSSRSSTKRKSRLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLSKKKLEAP -----TERHFSLRMK --
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ilarity 23.5%;
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47555 MW;
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No. 1.2e-05;
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                                                                                               DIMERIZATION WITH ANOTHER AHR, WITH HIF1A AS WELL A
                                                                                AHR, WITH HIF
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Pfam; PF00010; HLH; 1.
Pfam; PF000989; PAS; 2.
PRINTS; PR00785; NCTRNSLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00353; HCH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX; LOOP_HELIX; 1.
PROSITE; PS00038; HELIX; LOOP_HELIX; 1.
Nuclear protein; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as for modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
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EMBL; U14333; AAA61732.1; -.
HSSP; P22415; 1AN4.
MGD; MGI:88071; Arnt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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InterPro; IPR001092; HLH_dim.
InterPro; IPR001067; Nuctrnsl
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                                                                                                                                           130
                                                                                                                                                                       140
315 WPPAGVSLPDDDPEAGQGSKFCLVAI 340
                         212 YKPPAQTSPAGSPRS-EPPLQCLVLI 236
                                                                                                                195
                                                                                                                                                                                        74 GKRGRATGRILPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLCSSSLI----HNPT
                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                  PGTNF-SLELIGHSIFDFIHPCDQEELQDALTPRPN-LSKKKLEAPT------
                                                                                                                                                                                                                             LARENHSEIERRRRNKMTAYITELSDMVPTCSALARKPDKLTILRMAVSHM------
                                                        MCMGSRRSFICRMRCGTSSVDPVSMNRLSFLRNRCRNGLGSVKEGEPHFVVVHCTGYIKA
                                                                                   -----ERHFSLRMKSTLTS-------RGRTLNLKAAT-----WKVLHCSGHMRA 211
                                                                                                               PVLNOPQSEWFGSTLYDQVHPDDVDKLREQLSTSENALTGRVLDLKTGTVKKEGQQSSMR 254
                                                                                                                                                                      -KSLRGTGNTSTDGSYKPSFLTDQELKHLI----LEAADGFLFIVSCETGRVVYVSDSVT 194
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Pred. No. 0.00021;
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S -> T (IN REF. 2).

A -> R (IN REF. 2).

T -> S (IN REF. 2).

A -> C (IN REF. 2).

BDEB79E4BD75D452 CRC64;
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PAS 2.
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                                                                                                                                                                                                                                                                                                                Length 791;
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095k34 homo sapien
09jhs2 rattus norv
09jhs2 rattus norv
09yhn7 homo sapien
09hai2 homo sapien
09hai5 homo sapien
09hai5 bomo sapien
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09rib9 gallus gall
09xta5 bos taurus
035800 rattus norv
09cya8 mus musculu
056pt9 homo sapien
09upb1 homo sapien
09upb1 homo sapien
09utus rattus norv
09jhs1 rattus norv
09y7c6 gallus gall
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ALIGNMENTS

RESULT

Q9QX54 PRELIMINARY; PRT; 630 AA. Q9QX54; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOXIA-INDUCIBLE FACTOR 3 ALPHA (FRAGMENT).

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Bradfield C.A.;

HIF3A.

NCBI_TaxID=10090;

SEQUENCE FROM N.A. Gu Y.-Z., Moran S.M.,

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ID DORRER REPRESENTATION OF THE PROPERTY OF TH
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                                                                                                            InterPro;
InterPro;
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IPR003015;
IPR001067;
IPR001610;
                                            ; HLH_dim.
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Nuctrnslocator.
PAC.
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Q9WTU9 Q9JHS1 Q9W7C6

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                                                 PRINTS; PRO0785; NCTRNSLOCATR.

SMART; SM00353; HLH; 1.

SMART; SM00086; PAC; 1.

SMART; SM00091; PAS; 2.

PROSITE; PRO0038; HELIX, LOOP HELIX; UNKNOWN_1.

SEQUENCE 662 AA; 73013 MW; 58740A1B6993D3B5
                                                                                                         Pfam;
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EMBL; AF060194; AAC72734.1; -.
MGD; MGI:1859778; Hif3a.
                                                                                                                                                                                             Gu Y.Z., Moran S.M., Hogenesch J.B., Wartman L., Bradfield "Molecular characterization and chromosomal localization of alpha-class hypoxia induced factor subunit, HIF3alpha.";
                                                                                                                                                 InterPro;
InterPro;
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SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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SEQUENCE 630 AA; 69624 MW; 828EB2CB4E6D45E
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PRINTS; PR00785;
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                                                                                                         Pro; IPR000014; PAS. PF00989; PAS; 2.
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             Similarity
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IPR003015; HLH_Myc.
IPR001067; Nuctrnslocator.
IPR001610; PAC.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ14819 FIS, CLONE OVARC100241, MODERATELY SIMILAR
HYPOXIA-INDUCIBLE FACTOR 1 ALPHA.
HOMO Sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID-9806;
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ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
Masuho Y., Kanebori K.;
"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOZ7725; BAB55324.1;
SEQUENCE 632 AA; 68934 MW; A19F1ED3D05E7A71 CRC64;
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68.2%;
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                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 831; DB 4;
Pred. No. 3.8e-75;
l; Mismatches 30
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RESULT
Q9Y2N7
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Q9JHS2
  OC GRED DI DI CO
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Best I
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EMBL: AJ277827: CAB96611.1; -
InterPro; IPR001092; HLH_dim.
InterPro; IPR003015; HLH_Myc.
InterPro; IPR001067; Nuctrnslocator.
InterPro; IPR0010610; PAC.
InterPro; IPR0010610; PAC.
InterPro; IPR0000614; PAS.
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                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE HOMOLOG OF HYPOXIA (HYPOXIA-INDUCIBLE FACTOR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HTPOXIA INDUCIBLE FACTOR 3 ALPHA.
                                              HIF-3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
  Eukaryota; Metazoa;
                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSSTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SM00353; HLH;
; SM00086; PAC;
; SM00091; PAS;
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                                                                                                                                                                                                                PRELIMINARY;
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; 72887 MW; AC9672E340544010 CRC64;
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Rodentia;
Chordata;
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68.1%;
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                                                                  , Created)
, Last sequence update)
, Last annotation update)
A INDUCIBLE FACTOR THREE AI
3 ALPHA).
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Pred. No. 4.6e-74;
Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; 1
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                             ALPHA
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; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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RESULT
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Best Loc
Matches
Q9HAI2 PRELIMINARY; P
Q9HAI2;
01-MAR-2001 (TrEMBLrel. 16, Las
01-MAR-2001 (TrEMBLrel. 18, Las
01-OCT-2001 (TrEMBLrel. 18, Las
HYPOTHETICAL 70.0 KDA PROTEIN.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003015; HLH_Myc.
InterPro; IPR001067; Nuctrnslocator.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAS.
InterPro; IPR0010014; PAS.
Pfam; PF00989; PAS; 2.
PRINTS; PR00785; NCTRNSLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00096; PAG; 1.
SMART; SM000991; PAS; 2.
SMART; SM000991; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of human hypoxia-inducible factor-3 a. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AC007193; AAD22668.1; -. EMBL; AB054067; BAB69689.1; -. InterPro; IPR001092; HLH-dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stliwagen & Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Sarnes J., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J. Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J. Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olsen A.S., Carrano A.V.; "Sequence analysis of a 1 D19S412.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                               237
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Local 5
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                                                                                                                                                                                                                                                                                              DLCSSSLIHNPTPGTNFS-LELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPTER 176
                                                                                                                                                                                                                                                                                                                                                                                                                            RSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHR 68
                                                                                                                                                                                                     CEAIPQLPFHDGA 249
                                                                                                                                                                                                                                          HFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLI
                                                                                                                                                                                                                                                                                                                                                                                  LCAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQ-----QAPGPQSV 117
                                                                                                                                                                                                                                                                                                                                                                                                              RSTTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHR
                                                                                                                                                                                                                                                                                                                                                         LCAAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
667 AA; 72404 MW; 67B8794FF9DCCF4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
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                                          (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence up
(TrEMBLrel. 18, Last annotation
L 70.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                     229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 802; DB Pred. No. 3.4e 11; Mismatches
  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                   PRT;
                                                                                                                   648
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nes 28;
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                                                       on update)
  Hominidae;
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                   Euteleostomi;
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J.,
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RESULT RESULT I PRESULT I 
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Best Local Sin
Matches 104;
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Best Local :
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InterPro; IPR000014; PAS.
Pfam; PF00989; PAS; 2.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                        ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK021421; BAB13819.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-OCT-2001 (TrEMBLrel. 18, Last annotation
HYPOTHETICAL 21.6 KDA PROTEIN.
HOMO Sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSRRKVEAPTERCFSLRMKSTLTSRGRTLNLKAATWKVLNCSGHMRAYKPPAQTSPAGSP
     Conservative
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Primates;
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                             31.7%;
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     9,
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Score 518.5; DB (
Pred. No. 2.9e-44)
9; Mismatches 1:
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on update)
                                                       DB 4;
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                                                             199;
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  Gaps
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RESULT
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AC Q9
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Best Local :
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09XTA5 PRELIMI
09XTA5; 07:EMBI
01-NOV-1999 (TrEMBI
01-DEC-2001 (TrEMBI
HYPOXIA-INDUCIBLE I
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Q9YIB9;
01-MAY-1999
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cioning and expression of an avian cDNA for hypoxia-
inducible factor-1 alpha in embryonic ventricular myocytes.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB013746; BAA34234.2; -.

InterPro; IPR001092; HLH_dim.

InterPro; IPR001610; PAC.

InterPro; IPR000014; PAS.

InterPro; IPR000014; PAS.

SMART; SM00035; HLH; 1.

SMART; SM00086; PAC; 1.

SMART; SM00086; PAC; 1.

SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TREMBLrel. 10, Created)
01-OCT-2000 (TREMBLrel. 15, Last sequence up
01-DEC-2001 (TREMBLrel. 19, Last annotation
HYPOXIA-INDUCIBLE FACTOR-1 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                              172
                                                                                                                                                                               114
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                                                                                                                                                                                                                                                                                              KSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLICEAIP
                                                                                                                                                                                                                                                         LCAAGGKRGRAT-----GRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLCSSS 123
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                                                                                                                            ENVNKCMGLTQF--DLTGHSVFDFTHPCDHEELREMLTHRNGPVKKGKEQNTERSFFLRM
                                                                                                                                                                                                       LIHNPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPTERHFSLRM
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                                                                                                                                                                                                                                                                                                                                     119;
                                                                                                                                                                                                                                                                                                                                                 Similarity
(TTEMBLrel. 12, Created)
(TTEMBLrel. 12, Last sequence update)
(TTEMBLrel. 19, Last annotation update)
JCIBLE FACTOR-1 ALPHA.
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                   90542 MW;
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                                                                                                                                                                                                                                                                                                                                                 Score 503; DB 13; Pred. No. 6.2e-42;
                                                                 PRT;
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                                                                 823
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RESULT
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Best Local
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InterPro; IPR003015; HLH_Myc.
InterPro; IPR001321; Hypoxindf1A.
InterPro; IPR001610; pAC.
InterPro; IPR001610; pAC.
InterPro; IPR000014; PAS.
Pfam; PF00989; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PR01080; HYPOXIAIF1A.
SMART; SM00085; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX, LOOP_HELIX;
PROSITE; PS00038; HELIX, LOOP_HELIX;
                                                                                                                                                                                                                                                                                                                                                                  035800;
  MEDLINE=21134367; PubMed=11237857;
Kietzmann T., Cornesse Y., Brechte
"Perivenous expression of the mRNA
                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-99255430; PubMed-10320777;
Hara S., Kobayashi C., Imura N.;
"Molecular cloning of cDNAs encoding hypoxia-inducible factor (HIF)-lalpha and -2alpha of bovine arterial endothelial cells.";
Biochim. Biophys. Acta 1445:237-243(1999).
EMBL; AB018398; BAA78675.1; -.
                                                                                 SEQUENCE FROM N.A. STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                             HYPOXIA-INDUCIBLE FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQSQCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGDMIYISDNVNKYMGLTQF--ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSLIH-----NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           823 AA;
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX_LOOP_HELIX; UNKNOWN_1.
; 92127 MW; 12674E467A61B1A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46
  Y., Brechtel K., Mo of the mRNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 499;
Pred. No. 1.
                                                                                                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DLDIEDEMKAQMNCFYLKALDGFVMVLTD 105
                                                                                                                                                                                                                                                                                                                                                                                            825
  Modaressi S., Jungermann I
he three hypoxia-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
.6e-41
                                                                                                                                                                                   Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                 Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Q9CYA8
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
AA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S.,
AA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
AX Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
AX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
AX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
AX Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
AX Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
AX Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
AX Blake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F.,
AX Bushindich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
AX Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 113; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9CYA8 PRELIMINANA,
O9CYAB;
O1-JUN-2001 (TrEMBLrel. 17, Cr
O1-JUN-2001 (TrEMBLrel. 17, La
O1-DEC-2001 (TrEMBLrel. 19, La
TRIBUTCIBLE FACTOR 1, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PR01080; HYPOXIAIFIA.
SMART; SM00353; HLH; 1.
SMART; SM00085; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SEQUENCE 825 AA; 92319 MW; C4109A57F38667E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor a-subunits HIF-la, HIF2a and HIF3a in rat liver."; Biochem. J. 354:531-537(2001).
EMBL; Y09507; CAA70701.1; -.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001092; HLH_dim.
InterPro; IPR003015; HLH_Myc.
InterPro; IPR001321; HypoxindFlA.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRVRSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLVLICEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSLIHNPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPTERHFS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YISDNVNKYMGLTQF --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHRLCAAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKKKMSSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQSVDLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ELTGHSVFDFTHPCDHEEMREMLTHRNGPVRKGKEQNTQRSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 497; DB Pred. No. 2.5e Pred. No. 2.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 825;
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     P.,
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RESULT
Q96PT9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
Query Match
Best Local S
Matches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";

IL Nature 409:685-690(2001).

IR EMBL; AK017853; BAB30975.1; -.

IR MGD; MGI:106918; Hifla.

IN InterPro; IPR001092; HLH_dim.

IN InterPro; IPR003015; HLH_Myc.

IN InterPro; IPR003015; HLH_Myc.

IN InterPro; IPR001067; Nuctrnslocator.

IN InterPro; IPR001067; PAS.

IN INTERPO; IPR000014; PAS.

IN INTERPO; IPR003015; NCTRNSLOCATR.

SMART; SM00353; HLH; 1.

SMART; SM00351; PAS; 1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

SEQUENCE 258 AA; 29703 MW; C42D1CD68117C552 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-! Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
                                                                 Submitted (OCT-2001)
EMBL; AB073325; BAB7(
SEQUENCE 735 AA; (
                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOXIA-INDUCIBLE FACTOR 1 ALPHA VARIANT.
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                       tissue.";
                                                                                                                    Tanaka S., Sugimachi K.;
"Hypoxia-inducible factor-1 alpha variant isolated from
                                                                                                                                  Tanaka S.,
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                         Q96PT9
                                                                                                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                                                                                                                                                                               157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 44.1 nes 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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                                                                                                                                                                                                                                                                                                                                                                                                       PPLQCLVLICEAIP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                             KGKELNTQRSFELRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCG--YKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKLEAPTERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRVRSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLR
                                                                                                                                                                                                                                                                                                                                                                                            PPMTCLVLICEPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRKLLDAGGLDSEDEMKAQMDCFYLKALDGFVMVLTDDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHRLCAAGGKRGRATGR-------LLPEGPGGFRHGTHRRGRHGLPVGKC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKKKMSSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLR
 Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                 2001) to the EMBL/GenBank/DDBJ BAB70608.1; -. AA; 82746 MW; 34DD604FB4E4418
                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.3%;
            30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
 26;
            Score 495; DB 4; Length 735; Pred. No. 3.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 495; DB 11;
Pred. No. 9.4e-42;
9; Mismatches 61
                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                   34DD604FB4E4418E CRC64;
 Mismatches
                                                                                                                                                                                                                                                                                                                        735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                     Hominidae;
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                                                                                            databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                     Homo
                                                                                                                      human
48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K. -F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
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6
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Conservative

26;

Mismatches

59;

48;

Gaps

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RESULT
Q9UPB1
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                                                         δõ
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Query Match
Best Local Similarity
Matches 114; Conserv
                                                                                                                   InterPro; IPR001092; H.
InterPro; IPR003015; H.
InterPro; IPR001321; H.
InterPro; IPR001610; P.
InterPro; IPR001610; P.
InterPro; IPR000014; P.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UPB1;
Q9UPB1;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIF1A.
                                                                                                                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
HYPOXIA-INDUCIBLE FACTOR 1 ALPHA SUBUNIT.
                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           PRINTS; PRO1080; HYPOXIAIF1A.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                             evolutionary
                                                                                                                                                                                                                                                                                                                                                         "The
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99000835;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                             L; AF0501127; AAC68568.1;
AF0501115; AAC68568.1;
J; AF0501116; AAC68568.1;
J; AF050117; AAC68568.1; J
J; AF050118; AAC68568.1; J
                                                                                                                                                                                                                                                                                                                                                      N.V., Leung S.W., Semenza G.L., human hypoxia-inducible factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LICEPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICEAIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERHFSLRMKSTLTSRGRTLNLKAATWKVLHCSGHMRAYKPPAQTSPAGSPRSEPPLQCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGDMIYISDNVNKYMGLTQF--ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC
                                                                                                                                                                                            AF050123; AAC68568.1;
AF050124; AAC68568.1;
AF050125; AAC68568.1;
AF050126; AAC68568.1;
                                                                                                                                                                                                                                      AF050121;
AF050122;
                                                                                                                                                                                                                                                           AF050120;
                                                                                                                                                                                                                                                                     AF050119;
                                                       PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
826 AA; 92636 MW; ABD4F198A135BC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              conservation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                     AAC68568.1;
AAC68568.1;
AAC68568.1;
                                                                                                                                                                                                                                                                    ; AAC68568.1;
; AAC68568.1;
; AAC68568.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEAPT
                                                                                                                                                                                                                                                                                                                                                                PubMed=9782081;
                                                                                                                                         PAC.
               30.3%;
                                                                                                                                                                HypoxindF1A
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              Score 495; DB 4
Pred. No. 4e-41;
                                                                                                                                                                                                                                                                                                                                                                  .L.;
                                                                                                                                                                                                                                                                                                                                                        lalpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  826
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                         4.
                         Length 826;
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                                                                                                                                             Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                             Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00980; HYPOXIAIF1A.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                          PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Physiol. Genomics (Online) 6:159-168(2001). EMBL; AF057308; AAD24413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           Zou A.P., Yang Z.Z., Li P.L., Cowley AW J.R.; "Oxygen-dependent expression of hypoxia-inducible renal medullary cells of rats.";
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE DAWLEY; TISSUE-KIDN MEDLINE-21417706; PubMed-11526200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WTU9;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9WTU9
                                                                                                                                                                                                                                                                                                      InterPro; IPR000014; PAS
                                                                                                                                                                                                                                                                                                                   InterPro; IPR001321; HypoxindFla.
InterPro; IPR001610; PAC.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001092; HLH_dim.
InterPro; IPR003015; HLH_Myc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOXIA-INDUCIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164
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                                                                                                                                                Local Sin hes 113;
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                        119
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                                                                                            RSNTELRKEKSRDAARSRRSQETEVLYQLAHTLPFARGYSAHLDKASIMRLTISYLRMHR 68
| ::| ||||||||||||:::| |:|| || || ||:|||||:::
RMSSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRSFELRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCG--YKKPPMTCLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGDMIYISDNVNKYMGLTQF--ELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA-----PGPQSVDLC
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                      LCSSSLIH----
                                                                    LCAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQA------PGPQSVD
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                                                                                                                                                          Similarity
                                                                                                                                                                                                                     PS00038;
                                                                                                                                                                                                           823 AA;
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                                                                                                                                                                                                                                                                                                                                                                                          DAWLEY; TISSUE=KIDNEY;
                                                                                                                                                                                                         HELIX_LOOP_HELIX; UNKNOWN_1.
; 92116 MW; 0DC907B530766F1F CRC64;
            NPTPG-TNFSLELIGHSIFDFIHPCDQEELQDALTPRPNLSKKKLEA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACTOR-1 ALPHA.
                                                                                                                                                         30.0%;
                                                                                                                                             27;
                                                                                                                                            Score 491; DB 1
Pred. No. 1e-40;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                              DLDIEDEMKAQMNCFYLKALDGFVMVL
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                                                                                                                                             61;
                                                                                                                                                                     Length
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                                                                                                                                             Indels
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                                                                                                                                                                     823;
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В
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Best Local Sim
Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001092; HLH_Myc.

InterPro; IPR003015; HLH_Myc.

InterPro; IPR001610; Nuctrnslocator.

InterPro; IPR001610; PAC.

InterPro; IPR001610; PAC.

InterPro; IPR00014; PAS.

Pfam; PF00785; PAC; 1.

Pfam; PF00989; PAS; 2.

Pfam; PF00989; PAS; 2.

R PAINTS; PR00785; NCTRNSLOCATR.

R SMART; SM00353; HLH; 1.

R SMART; SM00036; PAC; 1.

R SMART; SM00091; PAS; 2.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

R PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21134367; PubMed-11237857; Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K "Perivenous expression of the mRNA of the three hypoxia-inducible factor a-subunits HIF-la, HIF2a and HIF3a in rat liver."; Biochem. J. 354:531-537(2001).

EMBL; AJ277828; CAB96612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Creat 01-OCT-2000 (TrEMBLrel. 15, Last 01-DEC-2001 (TrEMBLrel. 19, Last HYPOXIA INDUCIBLE FACTOR 2 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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223
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                                                                                            GDMIFLSENISKFMGLT-QVELTGHSIFDFTHPCDHEEIRENLTLKTGSGFGKKNKDRST
                                                                                                                                                                                                                       VDLCSSSLIHNPTPGTNFSLELIGHSIFDFIHPCDQEELQDALTPR--PNLSKKKLEAPT
                                                                                                                                                                                                                                                                                                                        ISYLRMHRL----CAAGGKRGRATGRLLPEGPGGFRHGTHRRGRHGLPVGKCQQAPGPQS 116
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Pred. No. 8.
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Search completed: September 8, 2002, 07:41:25 Job time: 443 sec

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